

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 792.231 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGTTT...AAAGTAGCATGCTGCCAG 141

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	141	100.0	383	9	AH013410S8	L42634 Homo sapien
2	141	100.0	3083	6	AR1444466	AR1444466 Sequence
3	141	100.0	3083	6	AR342446	AR342446 Sequence
4	139.4	98.9	2763	6	AR059583	AR059583 Sequence
5	139.4	98.9	2763	6	I28320	I28320 Sequence 1
6	139.4	98.9	2763	6	AR473576	AR473576 Sequence
7	139.4	98.9	2763	6	AR474046	AR474046 Sequence
8	139.4	98.9	168656	9	AL359922	AL359922 Human DNA
9	139.4	98.9	250000	9	AB060808	AB060808 Homo sapi
10	139.4	98.9	250000	2	AC109529	AC109529 Rattus no
11	64	45.4	225782	2	AC108638	AC108638 Rattus no
12	60.2	42.7	499	6	AR425810	AR425810 Sequence
13	60.2	42.7	499	6	AX986504	AX986504 Sequence
14	60.2	42.7	499	6	BD121363	BD121363 EST and e
15	60.2	42.7	1021	9	L40432	L40432 Homo sapien
16	60.2	42.7	1890	9	BC026106	BC026106 Homo sapi
17	60.2	42.7	2269	9	HSU2223	U22233 Human methy
18	56	39.7	194025	10	AL831719	AL831719 Mouse DNA
19	54.2	38.4	870	6	AX826996	AX826996 Sequence

20	48.4	34.3	313	6	AX915265	AX915265 Sequence
21	48.4	34.3	313	6	BD050798	BD050798 Sequence
22	45	31.9	1055	10	AB056100	AB056100 Mus muscu
23	45	31.9	2565	10	BC003858	BC003858 Mus muscu
24	44.6	31.6	144832	2	CR545471	CR545471 Danio rer
25	44.6	31.6	204824	2	CR388175	CR388175 Homo sapi
26	42.2	29.9	852	9	CR541670	CR541670 Homo sapi
27	39.2	27.8	849	9	CR541710	CR541710 Homo sapi
28	38.6	27.4	206136	9	AC068037	AC068037 Homo sapi
29	38.2	27.1	175561	9	AC012636	AC012636 Homo sapi
30	37.8	26.8	220885	2	AC095404	AC095404 Rattus no
31	37.8	26.8	243174	2	AC107550	AC107550 Rattus no
32	37.8	26.8	255300	2	AC128061	AC128061 Rattus no
33	36.8	26.1	246235	2	AC129432	AC129432 Rattus no
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36	36.4	25.8	246205	2	AC097898	AC097898 Rattus no
37	36.4	25.8	265477	2	AC099457	AC099457 Rattus no
38	36.2	25.7	229287	2	AC036172	AC036172 Homo sapi
39	36.2	25.7	240864	2	AC006510	AC006510 Homo sapi
40	36	25.5	176899	2	AC084108	AC084108 Mus muscu
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42	36	25.5	255220	2	AC122672	AC122672 Rattus no
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44	35.6	25.2	129241	9	AL353660	AL353660 Human DNA
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ALIGNMENTS

RESULT 1	AH013410S8	383 bp	DNA	linear	PRI 01-DEC-2003
LOCUS	AH013410S8				
DEFINITION	Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 8 and partial cds.				
ACCESSION	L42634	GI:38570314			
VERSION	L42634.1				
KEYWORDS	8 of 8				
SEGMENT	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 383)				
AUTHORS	Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.				
TITLE	Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)				
MEDLINE	96234115				
PUBMED	8650244				
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	/tissue_type="placenta"				
gene	order(L42627.1:1..199,L42628.1:1..316,L42629.1:1..190,L42630.1:1..280,L42631.1:1..441,L42632.1:1..567,L42633.1:1..303,1..383)				
	/gene="MTAP"				
mRNA	join(L42627.1:1..151,L42628.1:200..286,L42629.1:124..182,L42630.1:49..216,L42631.1:178..280,L42632.1:64..303,L42633.1:76..198,138..383)				
	/gene="MTAP"				
	/product="methylthioadenosine phosphorylase"				
CDS	join(L42627.1:119..151,L42628.1:200..286,L42629.1:124..182,L42630.1:49..216,L42631.1:178..280,L42632.1:64..303,L42633.1:76..198,138..176)				

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/note="putative"
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Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 54 AATCAAAATCTGGTTTCTTCTTCAACAACATCTCAGTAATTACGCCAATGTGAATAT 113
QY 61 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 120
DB 114 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 173
QY 121 TAAAGTAGCATGGCTGCCCAG 141
DB 174 TAAAGTAGCATGGCTGCCCAG 194

RESULT 2

AR144466

LOCUS AR144466 3083 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210917.
ACCESSION AR144466
VERSION AR144466.1 GI:15106333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3083)
AUTHORS Carson,D.A. and Carrera,C.J.
TITLE Method for suppressing multiple drug resistance in cancer cells
JOURNAL Patent: US 6210917-A 1 03-APR-2001;
FEATURES
source location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.2e-27;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2754 AATCAAAATCTGGTTTCTTCTTCAACAACATCTCAGTAATTACGCCAATGTGAATAT 2813
QY 61 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 120
DB 2814 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 2873
QY 121 TAAAGTAGCATGGCTGCCCAG 141
DB 2874 TAAAGTAGCATGGCTGCCCAG 2894

RESULT 3

AR342446
LOCUS AR342446 3083 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 25 from patent US 6576420.
ACCESSION AR342446
VERSION AR342446.1 GI:33737456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3083)
AUTHORS Carson,D.A., Schmid,M. and Carrera,C.J.
TITLE Method for early diagnosis of, and determination of prognosis in,
cancer
JOURNAL Patent: US 6576420-A 25 10-JUN-2003;
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source location/Qualifiers
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/mol_type="genomic DNA"

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Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2814 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 2873
QY 121 TAAAGTAGCATGGCTGCCCAG 141
DB 2874 TAAAGTAGCATGGCTGCCCAG 2894

RESULT 4

AR059583

LOCUS AR059583 2763 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5840505.
ACCESSION AR059583
VERSION AR059583.1 GI:5986033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
TITLE Method for inhibiting adenylosuccinate synthetase activity in
methylthioadenosine phosphorylase deficient cells
JOURNAL Patent: US 5840505-A 1 24-NOV-1998;
FEATURES
source location/Qualifiers
1..2763
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGGTTTCTTCTTCAACAACATCTCAGTAATTACGCCAATGTGAATAT 60
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QY 61 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 120
DB 2248 CACTGCCTCCTTCTTCTTCAGAATATGCCCCAGTTTCTGTTTATTACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCCAG 141
DB 2308 TAAAGTAGCATGGCTGCCCAG 2328

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128320
LOCUS      128320
DEFINITION Sequence 1 from patent US 5571510.
ACCESSION  128320
VERSION    128320.1 GI:1819096
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2763)
AUTHORS   Nobori,T. and Carson,D.A.
TITLE     Method for selective methionine starvation of malignant cells in
          mammals
JOURNAL   Patent: US 5571510-A 1 05-NOV-1996;
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SOURCE    1. .2763
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Best Local Similarity 99.3%; Pred. No. 1.7e-26;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB      2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY      61 CACTGCTCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 120
          |||
DB      2248 CACTGCTCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 2307
QY      121 TAAAGTAGCATGGCTGCCCAG 141
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DB      2308 TAAAGTAGCATGGCTGCCCAG 2328

RESULT 6
AR473576
LOCUS      AR473576
DEFINITION Sequence 14 from patent US 6689561.
ACCESSION  AR473576
VERSION    AR473576.1 GI:42711901
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2763)
AUTHORS   Carson,D.A. and Nobori,T.
TITLE     Tumor suppressor gene and methods for detection of cancer,
          monitoring of tumor progression and cancer treatment
JOURNAL   Patent: US 6689561-A 14 10-FEB-2004;
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DB      2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY      61 CACTGCTCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 120
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QY      121 TAAAGTAGCATGGCTGCCCAG 141
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DB      2308 TAAAGTAGCATGGCTGCCCAG 2328

RESULT 7
AR474046
LOCUS      AR474046
DEFINITION Sequence 14 from patent US 6689864.
ACCESSION  AR474046
VERSION    AR474046.1 GI:42712799
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2763)
AUTHORS   Carson,D.A. and Nobori,T.
TITLE     Cyclin dependent kinase 4 inhibitor
JOURNAL   Patent: US 6689864-A 14 10-FEB-2004;
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DB      2248 CACTGCTCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 2307
QY      121 TAAAGTAGCATGGCTGCCCAG 141
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DB      2308 TAAAGTAGCATGGCTGCCCAG 2328
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RESULT 8
AL359922
LOCUS      AL359922
DEFINITION Human DNA sequence from clone RP11-70L8 on chromosome 9, complete
          sequence.
ACCESSION  AL359922
VERSION    AL359922.10 GI:12191425
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 168656)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          laird,G.
JOURNAL   Direct Submission
          Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
          requests: clonerequest@sanger.ac.uk
          On Jan 13, 2001 this sequence version replaced gi:11878000.
          During sequence assembly data is compared from overlapping clones.
          Where differences are found these are annotated as variations
          together with a note of the overlapping clone name. Note that the
          variation annotation may not be found in the sequence submission
          only a small overlap as described above.
          This sequence has been finished according to sequence map criteria
          as follows. An attempt is made to resolve all sequencing problems,
          such as compressions and repeats, but not necessarily within known
          annotated repeat sequence elements. Where the sequence is
          ambiguous, there is an annotation using the 'unsure' feature key.
          The following abbreviations are used to associate primary accession
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numbers given in the feature table with their source databases:
Em:, EMBL, Sw:, SWISSPROT, Tr:, TREMBL, Wp:, WORMPEP, Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-70L8 is from the library RP11-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
This sequence is the entire insert of clone RP11-70L8 The true left
end of clone RP11-14912 is at 118787 in this sequence. The true
right end of clone RP11-47303 is at 73731 in this sequence.

FEATURES

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ORIGIN

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QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 119409 TAAAGTAGCATGGCTGCCAG 119429

RESULT 9

AB060808 250000 bp DNA linear PRI 26-APR-2002
LOCUS Homo sapiens gene for p16/CDKN2A, complete cds.
DEFINITION AB060808
ACCESSION AB060808.1 GI:20330501
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Kohno, T., Inoue, K., Kitagawa, Y., Hayashi, Y., Matsuo, Y.,
Mizoguchi, H. and Yokota, J.
Prevalent Involvement of Illegitimate V(D)J Recombination in
Chromosome 9p21 Deletions in Lymphoid Leukemia

Unpublished
2 (bases 1 to 250000)

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Yokota, J., Kohno, T., Inoue, K. and Kitagawa, Y.
Direct Submission
Submitted (25-APR-2001) Takashi Kohno, National Cancer Center
Research Institute, Biology Division; 1-1, Tsukiji 5-chome,

Chuo-Ku, Tokyo 104-0045, Japan (E-mail: tckohno@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4652), Fax:81-3-3542-0807)

FEATURES

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ORIGIN

Query Match 98.9%; Score 139.4; DB 9; Length 250000;
Best Local Similarity 99.3%; Pred. No. 8e-27;
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RESULT 10

AC109529 225782 bp DNA linear HTG 15-NOV-2002
LOCUS Rattus norvegicus clone CH230-276K5, *** SEQUENCING IN PROGRESS
DEFINITION AC109529
ACCESSION AC109529.5 GI:25006711
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM

REFERENCE

1 (bases 1 to 225782)

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Derramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Query Match	42.7%;	Score 60.2;	DB 6;	Length 499;
Best Local Similarity	89.0%;	Pred. No. 1.3e-05;		
Matches	65;	Conservative	0;	Mismatches 8; Indels 0; Gaps 0;

OY	69	CCTTTCCTCCCTTCAGAAATATGGCCCAAGTTTCTGTTTATTATACCAAGACATTAAAGTAG	128
Db	343	CCTCCATAACCTGAAGAATATGGCCCAAGTTTCTGTTTATTATACCAAGACATTAAAGTAG	402

OY	129	CATGGCTGCCCAG	141
Db	403	CATGGCTGCCCAG	415

RESULT 13				
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LOCUS	AX986504	499 bp	DNA	linear
DEFINITION	Sequence 17307 from Patent EP1104808.			PAT 15-JAN-2004
ACCESSION	AX986504			
VERSION	AX986504.1	GI:40992644		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

REFERENCE	1	
AUTHORS	Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.	
TITLE	ESTs and encoded human proteins	
JOURNAL	Patent: EP 1104808-A 17307 06-JUN-2001;	
	Genset (FR)	

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Query Match	42.7%;	Score 60.2;	DB 6;	Length 499;
Best Local Similarity	89.0%;	Pred. No. 1.3e-05;		
Matches	65;	Conservative	0;	Mismatches 8; Indels 0; Gaps 0;

OY	69	CCTTTCCTCCCTTCAGAAATATGGCCCAAGTTTCTGTTTATTATACCAAGACATTAAAGTAG	128
Db	343	CCTCCATAACCTGAAGAATATGGCCCAAGTTTCTGTTTATTATACCAAGACATTAAAGTAG	402

OY	129	CATGGCTGCCCAG	141
Db	403	CATGGCTGCCCAG	415

RESULT 14				
BD121363				
LOCUS	BD121363	499 bp	DNA	linear
DEFINITION	EST and encoded human protein.			PAT 18-SEP-2002
ACCESSION	BD121363			
VERSION	BD121363.1	GI:23216273		
KEYWORDS	JP 2002010789-A/13440.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

REFERENCE	1	
AUTHORS	Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.	
TITLE	EST and encoded human protein	
JOURNAL	Patent: JP 2002010789-A 13440 15-JAN-2002;	
	GENSET CORP	

COMMENT	OS	Homo sapiens (human)
	PN	JP 2002010789-A/13440
	PD	15-JAN-2002
	PF	07-AUG-2000 JP 2000280989
	PR	05-AUG-1999 US 60/147499
	PI	JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
		GIORDANO

```

PC      C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC      C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
C12N15/00
CC      EST and encoded human protein
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FT      source      1..499
FT      Location/Qualifiers
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ORIGIN
Query Match      42.7%; Score 60.2; DB 6; Length 499;
Best Local Similarity 89.0%; Pred. No. 1.3e-05;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db      343 CCTCCATAACCTGAAGAATATGGCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 402
QY      129 CATGGCTGCCAG 141
        ||| | | | | | | | |
Db      403 CATGGCTGCCAG 415

RESULT 15
L40432      1021 bp      mRNA      linear      PRI 12-DEC-2000
LOCUS      Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
DEFINITION      complete cds.
ACCESSION      L40432
VERSION      L40432.1 GI:11602391
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1021)
AUTHORS      Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
TITLE      Genomic cloning of methylthioadenosine phosphorylase: a purine
            metabolic enzyme deficient in multiple different cancers
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)
MEDLINE      96234115
PUBMED      8650244
REFERENCE      2 (bases 1 to 1021)
AUTHORS      Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.
            and Carson,D.A.
TITLE      Direct Submission
JOURNAL      Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
            Research on Aging, and Department of Medicine, University of
            California at San Diego, La Jolla, CA 92093-0663, USA
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            [Flatfile retrieved from GSDS Thu Dec 7 15:18:48 2000].
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SVLLPRH"

ORIGIN

Query Match	42.7%;	Score 60.2;	DB 9;	Length 1021;
Best Local Similarity	89.0%;	Pred. No. 1.1e-05;		
Matches 65;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	69	CCTTCTCCTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAAGTAG	128	
Db	908	CCTCCATACTGAAGATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAAGTAG	967	
QY	129	CATGGCTGCCAG	141	
Db	968	CATGGCTGCCAG	980	

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Job time : 796.231 secs

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PN	WO9920791-A1.
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PD	29-APR-1999.
XX	
PF	23-OCT-1998; 98WO-US022557.
XX	
PR	23-OCT-1997; 97US-00956657.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Carson DA, Cottam HB, Nobori T, Carrera CJ,
XX	
DR	WPI; 1999-302753/25.

PT Suppression of multiple drug resistance in cells, for treatment of, e.g. leukemia's.
PT

PS Example 3; Page 42-44; 45pp; English.

CC This is the DNA sequence of a human methylthioadenosine phosphorylase
CC (MTase) genomic DNA clone that was isolated from a cosmid gene library
CC using an MTase cDNA probe. The encoded enzyme catabolises
CC methylthioadenosine to adenine for endogenous salvage incorporation into
CC the intracellular AMP pool. The invention relates to methods for treating
CC and preventing the onset and maintenance of multiple drug resistance
CC (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC cells are depleted of AMP and ATP and are thus unable to supprt P-
CC glycoprotein activity. One method obtains a population of target cells
CC from a host and assays for loss of MTase activity. MTase deficient cells
CC are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC starves the cells of adenine and suppresses P-glycoprotein activity. The
CC MTase deficient host cells are preferably primary tumour cells comprising
CC small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC cells or urothelial tumor cells, preferably in humans. MTase competent
CC cells are also treated for MDR with purine synthesis inhibitors. MTase
CC competent and deficient cells are also treated for malignancy with other
CC anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC to detect the presence or absence of MTase in malignant cell lines
XX
SQ Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;

Query Match	100.0%;	Score 141;	DB 2;	Length 3083;
Best Local Similarity	100.0%;	Pred. No. 4.4e-31;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AATCAAAATCTGTTTTTTTTTAAACAACATCTCAGTAATTAAGCCCAACATGTGAATAT 60
DB 2754 AATCAAAATCTGTTTTTTTTTAAACAACATCTCAGTAATTAAGCCCAACATGTGAATAT 2813
QY 61 CACTGCCTCCCTTCTCTCCCTTTCAGAAATATGCCAGTTTTCTGTATTATTAACCAAGACAT 120

Db	2814 CACTGCCCTCCCTTCTTCCTTTCAGAATATGGCCCCAGTTTCTGTGTTTATTACCAAGACAT 2873
Oy	121 TAAAGTAGCATGGCTGCCAG 141
Db	2874 TAAAGTAGCATGGCTGCCAG 2894

RESULT 2
ABX10818
ID ABX10818 standard; DNA; 3083 BP.
XX
AC ABX10818;
XX
DT 17-APR-2003 (first entry)
XX
DE DNA encoding rat methylthioadenosine phosphorylase (MTase).
XX
KW Rat; methylthioadenosine phosphorylase; MTase; detection;
KW Rangione method; gene; ds.
XX
OS Rattus sp.

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FT	exon	724..782
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FT	exon	899..1066
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PN		US2002146695-A1.
XX		
PD	10-OCT-2002.	
XX		

PF 09-FEB-2001; 2001US-00780114.
XX
PR 29-DEC-1993; 93US-00176855.
PR 02-JUN-1995; 95US-00459343.
PR 04-MAY-1998; 98US-00072914.
XX
PA (NOBO/) NOBORI T.
PA (CARs/) CARSON D. A.
PA (TAKA/) TAKABAYASHI K.
XX
PI Nobori T, Carson DA, Takabayashi K;
XX
DR WPI; 2003-208976/20.
XX
PT Detection of methylthioadenosine phosphorylase presence in mammalian
PT cells, by adding to sample oligonucleotide probes capable of hybridizing
PT to methylthioadenosine phosphorylase encoding nucleic acid.
XX
PS Claim 7; Fig 1; 16pp; English.
XX
CC The invention describes a method of detecting methylthioadenosine
CC phosphorylase (MTase) comprising adding oligonucleotide probes
CC hybridisable to MTase encoding nucleic acid to an assayable sample of
CC cells, where the presence of the nucleic acid indicates the presence of
CC the MTase in a cell. The inventive method is simple and efficient in
CC detecting the presence of MTase in the mammalian cell. The availability
CC of the recombinant MTase enables the production of highly pure material
CC with greater ease and in greater quantities than was obtained using
CC Rangione method for the isolation and purification of native MTase. This
CC sequence encodes rat methylthioadenosine phosphorylase (MTase)
XX
SQ Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

Query Match 100.0%; Score 141; DB-8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 4.4e-31;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCCAACATGTGAATAT 60
Db 2754 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCCAACATGTGAATAT 2813

QY 61 CACTGCCTCTTCTTCTTCTTCAAGATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 120
Db 2814 CACTGCCTCTTCTTCTTCTTCAAGATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 2873

QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2874 TAAAGTAGCATGGCTGCCAG 2894

RESULT 3
AAT15167
ID AAT15167 standard; DNA; 2763 BP.
XX
AC AAT15167;
XX
DT 29-JUN-1996 (first entry)
XX
DE Methylthioadenosine-phosphorylase gene.
XX
KW Human; methylthioadenosine-phosphorylase; chromosome walking;
KW interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW antibody; imaging; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254..421
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FT Intron 422..615

FT /*tag= c
FT exon 616..720
FT /*tag= d
FT Intron 721..963
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FT exon 964..1203
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XX
XX WO9528169-A1.
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XX 26-OCT-1995.
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XX 12-APR-1995; 95WO-US004655.
XX
XX 14-APR-1994; 94US-00227800.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Carson DA, Nobori T;
XX
XX WPI; 1995-373630/48.
XX
XX Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT useful for diagnosis, assessing predisposition and treatment of cancers.
XX
XX Example 1; Page 96-101; 129pp; English.
XX
XX The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC tumour suppressor gene (AAT15157-58) is located between this gene and an
CC interferon-alpha gene cluster, and has been isolated by chromosome
CC walking. The CDK4I gene, probe and primer derivatives and the gene
CC product may be used in diagnosis of cancer, particularly melanoma
CC (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC or in antitumour antisense oligonucleotide or ribozyme construction.
CC Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCCAACATGTGAATAT 2247

QY 61 CACTGCCTCTTCTTCTTCTTCAAGATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 120
Db 2248 CACTGCCTCTTCTTCTTCTTCAAGATATGCCCCAGTTTCTGTTTATTATTAACAAGACAT 2307

QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 4
AAQ92813
ID AAQ92813 standard; DNA; 2763 BP.
XX
AC AAQ92813;
XX
DT 25-MAR-2003 (revised)
DT 05-DEC-1995 (first entry)
XX
DE Human MTase.
XX
KW MTase; methyladenosine-phosphatase; malignancy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

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FT exon 254..421
FT /tag= a
FT exon 616..720
FT /tag= b
FT exon 964..1203
FT /tag= c
FT exon 1640..1762
FT /tag= d
FT exon 2272..2310
FT /tag= e
XX
XX WO9518233-A1.
XX
XX 06-JUL-1995.
XX
XX 22-DEC-1994; 94WO-US014920.
XX
XX 29-DEC-1993; 93US-00176855.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (CIBA ) CIBA GEIGY CORP.
XX
XX Nobori T, Carson DA, Takabayashi K;
XX
XX WPI; 1995-246398/32.
XX
XX Detecting methyl:adenosine phosphatase in mammalian cells - by
XX PT hybridisation with specific oligonucleotide for detecting malignancy,
XX PT also new nucleic acid, expression vectors, derived polypeptide(s) and
XX PT antibodies.
XX
XX Claim 8; Page 34-35; 47pp; English.
XX
XX A cosmid gene library constructed from human placenta DNA was screened
XX CC using a MTase cDNA probe to isolate a human MTase genomic clone (sequence
XX CC given in AAQ92813). Absence of MTase from a cell is indicative of
XX CC malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;
SQ

Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 2247

QY 61 CACTGCCTCCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
Db 2248 CACTGCCTCCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307

QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 5
AAT85305
ID AAT85305 standard; DNA; 2763 BP.
XX
XX AAT85305;
AC
XX
XX 28-FEB-1998 (first entry)
XX
XX Human methylthioadenosine phosphorylase.
DE
XX
XX Methylthioadenosine phosphorylase; MTase; human;
KW adenylosuccinate synthetase; lung cancer; glioma;
KW acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
XX Homo sapiens.
XX
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FH Key Location/Qualifiers
FT exon 254..421
FT /tag= a
FT /number= 1
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FT intron 721..963
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FT /number= 3
XX
XX WO9732994-A1.
XX
XX 12-SEP-1997.
XX
XX 27-JAN-1997; 97WO-US001193.
XX
XX 08-MAR-1996; 96US-00612542.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
XX WPI; 1997-470550/43.
XX
XX Inhibiting adenylosuccinate synthetase activity in methylthio:adenosine
XX PT phosphorylase-deficient cells - by treatment with specific inhibitor,
XX PT especially L-alanosine, useful for selective killing of MTase deficient
XX PT cancer cells.
XX
XX Example 3; Page 25-26; 37pp; English.
XX
XX This DNA sequence comprises human genomic DNA for methylthioadenosine
XX CC phosphorylase (MTase), obtained from a cosmid gene library constructed
XX CC from human placenta DNA by screening with a MTase cDNA probe. A claimed
XX CC method for inhibiting the activity adenylosuccinate synthetase (ASS) in
XX CC mammalian cells deficient in MTase activity involves: (a) determining
XX CC that a population of cells obtained from a mammalian host is MTase
XX CC deficient; and (b) administering an ASS inhibitor (preferably L-
XX CC alanosine) to the host so that the MTase deficient host cells are
XX CC depleted of AMP. The method is especially used to treat human MTase-
XX CC deficient primary tumour cells, specifically non-small cell lung cancer,
XX CC acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
XX CC MTase catabolises methylthioadenosine to adenine for endogenous salvage
XX CC incorporation into the intracellular AMP pool. The claimed method
XX CC deprives the cells of substrate for de novo synthesis of AMP, resulting
XX CC in selective killing of these cells. MTase sequence-specific
XX CC oligonucleotides can be used to detect the presence or absence of MTase in
XX CC malignant cell lines
XX
XX Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;
SQ

Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 2247

QY 61 CACTGCCTCCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
Db 2248 CACTGCCTCCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307

QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2308 TAAAGTAGCATGGCTGCCAG 2328
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RESULT 6
AAZ00866
ID AAZ00866 standard; DNA; 2763 BP.
XX
AC AAZ00866;
XX
DT 20-OCT-1999 (first entry)
XX
DE Human MTase DNA.
XX
KW MTase; methylthioadenosine phosphorylase; human; detection; active;
KW catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS Homo sapiens.
XX
FH Key
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FT /tag= a
FT /number= 1
FT /note= "Putative exon"
FT 422. .615
FT /tag= b
FT /number= 1
FT /note= "putative intron"
FT 616. .720
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FT /number= 2
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FT 964. .1203
FT /tag= e
FT /number= 3
FT /note= "putative exon"
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XX
PD 24-AUG-1999.
XX
PF 18-DEC-1996; 96US-00772113.
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Takabayashi K, Carson DA, Nobori T;
XX
DR WPI; 1999-507775/42.
XX
PT Detecting catalytically active and inactive methylthioadenosine
PT phosphorylase (MTase) in mammalian cells useful for identifying malignant
PT cells which are suitable targets for methionine (MET) starvation therapy.
XX
PS Claim 6; Fig 1; 14pp; English.
XX
CC This invention describes a novel method for detecting catalytically
CC active and inactive methylthioadenosine phosphorylase (MTase) in
CC mammalian cells, using oligonucleotide probes which hybridize to MTase
CC nucleic acid coding regions. Detection of MTase encoding nucleic acid
CC indicates the cell has catalytically active MTase. The method is useful
CC for detecting malignant cells with a deficient MTase gene, useful for
CC identifying malignant cells which are suitable targets for methionine
CC (MET) starvation therapy. The new method is simple, efficient and
CC successful at determining MTase negative cells, unlike prior art
CC techniques, which include analysis of catalytic activity in cell
CC cultures, requiring a commercially unavailable radiochemical substrate,
CC and immunoassays, using MTase antibodies which are unable to be produced
CC in sufficient quantities. Recombinant MTase protein produced using the
CC new polynucleotide and vector, allows greater and purer production of

CC MTase than prior art techniques (using the Rangione method) for isolating
CC native MTase. This sequence represents human MTase encoding DNA which is
CC used in the method of the invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;
Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAATGTGAATAT 60
DB 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAATGTGAATAT 2247
QY 61 CACTGCCCTCCTTCTTCTTCTTCAAGATATGCCAGTTTCTGTTTATTACCAAGACAT 120
DB 2248 CACTGCCCTCCTTCTTCTTCTTCAAGATATGCCAGTTTCTGTTTATTACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
DB 2308 TAAAGTAGCATGGCTGCCAG 2328
RESULT 7
AAF86091
ID AAF86091 standard; DNA; 2763 BP.
XX
AC AAF86091;
XX
DT 06-JUL-2001 (first entry)
XX
DE Methylthioadenosine phosphorylase.
XX
KW Methylthioadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW cancer; ds.
XX
OS Unidentified.
XX
PN US6214571-B1.
XX
PD 10-APR-2001.
XX
PF 24-NOV-1998; 98US-00199137.
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
DR WPI; 2001-315458/33.
XX
PT Inhibiting adenine succinate synthetase (ASS) activity in
PT methylthioadenosine phosphorylase deficient cells of mammalian host
PT involves administering ASS inhibitor which depletes adenosine 5'
PT monophosphate in cells.
XX
PS Disclosure; Fig 1; 17pp; English.
XX
CC The present invention relates to inhibiting adenyl succinate synthetase
CC (ASS) activity in methylthioadenosine phosphorylase (MTase) deficient
CC cells of mammalian host. The invention may be used as a treatment for
CC cancer, especially breast and colon cancer
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;
Query Match 98.9%; Score 139.4; DB 5; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAATGTGAATAT 60
DB 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAATGTGAATAT 2247

QY 61 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
|||||
Db 2248 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
|||||
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 8
AAD64097
ID AAD64097 standard; DNA; 2763 BP.
XX
AC AAD64097;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human methylthioadenosine phosphorylase (MTase) genomic DNA.
XX
KW Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTase;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH exon 254..421
FT /*tag= a
FT 422..615
FT intron /*tag= b
FT 616..720
FT exon /*tag= c
FT 721..963
FT intron /*tag= d
FT exon 964..1203
FT /*tag= e

XX
PN US2003138928-A1.
XX
PD 24-JUL-2003.
XX
PF 18-JUL-2001; 2001US-00908671.
XX
PR 26-AUG-1997; 97US-00921954.
XX
PA (CARS/) CARSON D A.
PA (NOBO/) NOBORI T.
XX
PI Carson DA, Nobori T;
XX
DR WPI; 2003-851737/79.
XX
PT New isolated polynucleotide encoding cyclin-dependent kinase 4l, useful
PT for preparing a composition for diagnosing or treating cancer.
XX
PS Example 1; SEQ ID NO 14; 46bp; English.
XX
CC The present invention relates to novel tumour suppressor genes, termed as
CC cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC proteins. The polynucleotides are useful for preparing a composition for
CC diagnosing or treating cancer. Sequences of the invention are also useful
CC in gene therapy. The present sequence is human methylthioadenosine
CC phosphorylase (MTase) genomic DNA used in the exemplification of the
CC invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 98.9%; Score 139.4; DB 10; Length 2763;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60

Db 2188 AATCAAAATCTGTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
|||||
QY 61 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
|||||
Db 2248 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
|||||
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 9
AAQ99202
ID AAQ99202 standard; DNA; 2784 BP.
XX
AC AAQ99202;
XX
DT 07-MAR-1996 (first entry)
XX
DE Pseudomonas putida methylthioadenosine-phosphorylase DNA.
XX
KW Enzyme; MTase; L-Met-L-deamino-gamma-mercaptopmethane-lyase;
KW chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS Pseudomonas putida.
XX
FH Key Location/Qualifiers
FH CDS 1..2763
FT /*tag= a

XX
PN WO9517908-A1.
XX
PD 06-JUL-1995.
XX
PF 22-DEC-1994; 94WO-US014919.
XX
PR 29-DEC-1993; 93US-00176413.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Nobori T, Carson DA;
XX
DR WPI; 1995-246192/32.
XX
PT Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT negative tumour cells - used in chemotherapy of mammalian malignant
PT cells.
XX
PS Disclosure; Page 27-28; 46pp; English.
XX
CC Antigenic peptides may be generated from this sequence encoding
CC methyladenosine-phosphorylase, which are then used to generate antibodies
CC specific for MTase. The produced antibodies may be used in an immunoassay
CC for the detection of MTase
XX
SQ Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

Query Match 98.9%; Score 139.4; DB 2; Length 2784;
Best Local Similarity 99.3%; Pred. No. 1.2e-30;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
|||||
Db 2188 AATCAAAATCTGTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
|||||
Db 2248 CACTGCCTCCTTCTCTTCAGATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
|||||
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

```
RESULT 10
ABQ59540/c
ID ABQ59540 standard; cDNA; 603 BP.
XX
AC ABQ59540;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:3235.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
XX genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB ) BAYER CORP.
XX
PI Burgees C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiagalingam A, Lewis ME;
XX
DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridizes to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists
XX
SQ Sequence 603 BP; 159 A; 119 C; 110 G; 206 T; 0 U; 9 Other;
```

```
Query Match 43.8%; Score 61.8; DB 6; Length 603;
Best Local Similarity 96.9%; Pred. No. 3.2e-08;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 77 CCTTCAGATATGCCCCAGTTTCTGTTTATATACCAAGACATTAAGTAGCATGGCTG 136
DB 440 CCTTGAAGATATGCGCCAGTTTCTGTTTATATACCAAGACATTAAGTAGCATGGCTG 381
```

```
QY 137 CCCAG 141
DB 380 CCCAG 376
```

RESULT 11
AAH33683
ID AAH33683 standard; cDNA; 1437 BP.

```
XX
AC AAH33683;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:739.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 9; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
XX
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
XX
DR P-PSDB; AAG74252.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 1; Page 2728-2729; 9803pp; English.
```

```
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
```

```
SQ Sequence 1437 BP; 501 A; 202 C; 262 G; 460 T; 0 U; 12 Other;
```

```
Query Match 43.5%; Score 61.4; DB 4; Length 1437;
Best Local Similarity 89.0%; Pred. No. 5.1e-08;
Matches 65; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 69 CCTTCTTCTTTCAGATATGCCCCAGTTTCTGTTTATATACCAAGACATTAAGTAG 128
DB 104 CCTTCMTAACCTGAAGATATGCCCCAGTTTCTGTTTATATACCAAGACATTAAGTAG 163
```

```
QY 129 CATGGCTGCCAG 141
DB 164 CATGGCTGCCAG 176
```

RESULT 12
ADC30327
ID ADC30327 standard; cDNA; 2197 BP.
XX
AC ADC30327;
XX

Best Local Similarity 88.1%; Pred. No. 5.6e-06;
Matches 59; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 69 CCTTCTTCCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAAGTAG 128
DB 804 CCTCCATAACCTGAAGATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAAGTAG 863
QY 129 CATGGCT 135
DB 864 CATGGCT 870

RESULT 14
AAC27053
ID AAC27053 standard; cDNA; 313 BP.
AC AAC27053;
DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 31128.
XX
KM Human; 5' EST, expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 31128; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNA or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 313 BP; 99 A; 50 C; 68 G; 96 T; 0 U; 0 Other;

Query Match 34.3%; Score 48.4; DB 3; Length 313;
Best Local Similarity 98.0%; Pred. No. 0.00022;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTTTTTTTTAAACAACATCTCAGTAATTAGCCCAAC 50
DB 262 AATCAAAATCTGTTTTTTTTTAAACAACATCTCAGTAATTAGCCCAAC 311

RESULT 15
AAD55694
ID AAD55694 standard; DNA; 175561 BP.
XX
AC AAD55694;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human THBS4 reference gene (GI 14916146).
XX
KW Human; thrombospondin 4; THBS4; vascular disease; therapy; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT variation replace(105290,C)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace(118019,A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO2003020120-A2.
XX
PD 13-MAR-2003.
XX
PF 04-SEP-2002; 2002WO-US028281.
XX
PR 04-SEP-2001; 2001US-0317033P.
PR 17-OCT-2001; 2001US-0330248P.
PR 14-DEC-2001; 2001US-00017721.
XX
PA (VITI-) VITIVITY INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI McCarthy J, Daley G, Bolk S;
XX
DR WPI; 2003-312992/30.
XX
PT Novel isolated nucleic acid comprising allelic variant of polymorphic
PT region of thrombospondin 1 or 4 gene, useful for identifying
PT predisposition of subject to develop vascular disease associated with the
PT allelic variant.
XX
PS Claim 64; Fig 3; 338pp; English.
XX
CC The invention is based at least in part on the discovery of polymorphisms
CC within the thrombospondin 1 (THBS1) or THBS4 genes. The invention also
CC provides a nucleic acid comprising allelic variant of polymorphic region
CC of THBS1 or THBS4 gene. The method is useful for identifying a subject as
CC a candidate for a particular clinical course of therapy or to treat a
CC vascular disease or disorder and for selecting a clinical course of
CC therapy to treat a subject who is at risk for developing a vascular
CC disease or disorder. The present sequence is human THBS4 reference gene.
CC Note: This sequence is said to encode SEQ ID NO: 4 (AAE36229). However
CC this does not appear to be the case
XX
SQ Sequence 175561 BP; 51351 A; 37974 C; 36559 G; 49677 T; 0 U; 0 Other;

Query Match 27.1%; Score 38.2; DB 8; Length 175561;
Best Local Similarity 58.3%; Pred. No. 0.8;
Matches 67; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 9 TCTGTTTTTTTTTAAACAACATCTCAGTAATTAGCCCAACATGGAATATCACTGCT 68
DB 3596 TATGGTTTGTGTTTTTAAACAACCTCATCTTGAATGACTCTGCTGGAACCTAGCAT 3655
QY 69 CCTTCTTCCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACATTA 123
DB 3656 TTTTCTTCTTTCAGATATTCACATCTGTATATTAATTGACTAAGATTCA 3710

Search completed: February 1, 2005, 12:39:36
Job time : 188.045 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGTTT...AAAGTAGCATGCTGCCAG 141

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	100.0	3083	3	US-08-956-657-1 Sequence 1, Appl1
2	141	100.0	3083	4	US-09-335-231-25 Sequence 25, Appl1
3	139.4	98.9	2763	1	US-08-176-413-1 Sequence 1, Appl1
4	139.4	98.9	2763	2	US-08-612-542-1 Sequence 1, Appl1
5	139.4	98.9	2763	2	US-08-772-113-1 Sequence 1, Appl1
6	139.4	98.9	2763	3	US-09-199-137-1 Sequence 1, Appl1
7	139.4	98.9	2763	4	US-08-227-800A-14 Sequence 14, Appl1
8	139.4	98.9	2763	4	US-08-921-954-14 Sequence 14, Appl1
9	139.4	98.9	2763	5	PCT-US94-14919-1 Sequence 1, Appl1
10	139.4	98.9	2763	5	PCT-US94-14920-1 Sequence 1, Appl1
11	60.2	42.7	499	4	US-09-621-976-17307 Sequence 17307, A
12	48.4	34.3	313	4	US-09-513-999C-31128 Sequence 31128, A
13	32.4	23.0	1230025	4	US-09-198-452A-1 Sequence 1, Appl1
14	32	22.7	32	4	US-09-335-231-24 Sequence 24, Appl1
15	30.6	21.7	700	3	US-08-998-416-302 Sequence 302, App
16	30.6	21.7	714	3	US-08-998-416-863 Sequence 863, App
17	30.6	21.7	714	3	US-08-998-416-1139 Sequence 1139, App
18	30.6	21.7	722	3	US-08-998-416-680 Sequence 680, App
19	30.6	21.7	725	3	US-08-998-416-1051 Sequence 1051, App
20	30.6	21.7	761	3	US-08-998-416-382 Sequence 382, App
21	29.2	20.7	4612	4	US-09-626-301-1 Sequence 1, Appl1
22	29.2	20.7	4642	4	US-09-626-301-3 Sequence 3, Appl1
23	29	20.6	4261	4	US-09-976-594-3 Sequence 3, Appl1
24	28.8	20.4	3001	3	US-09-387-212-9 Sequence 9, Appl1
25	28.8	20.4	3001	4	US-09-948-802-9 Sequence 9, Appl1
26	28.8	20.4	3552	4	US-09-643-597-126 Sequence 126, App
27	28.8	20.4	3552	4	US-09-480-884A-126 Sequence 126, App

28	28.8	20.4	3552	4	US-09-542-615A-126	Sequence 126, App
29	28.8	20.4	3552	4	US-09-606-421B-126	Sequence 126, App
30	28.8	20.4	3552	4	US-09-221-107-126	Sequence 126, App
31	28.8	20.4	3552	4	US-09-466-396A-126	Sequence 126, App
32	28.8	20.4	3552	4	US-09-476-496A-126	Sequence 126, App
33	28.8	20.4	3552	4	US-09-630-940B-126	Sequence 126, App
34	28.6	20.3	1609	4	US-09-976-594-550	Sequence 550, App
35	28.6	20.3	2172	4	US-09-976-594-125	Sequence 125, App
36	28.6	20.3	5156	2	US-09-091-432-3	Sequence 3, Appl1
37	28.6	20.3	5156	4	US-09-387-663-3	Sequence 3, Appl1
38	28.6	20.3	5156	4	US-09-214-139B-3	Sequence 3, Appl1
39	28.6	20.3	5762	4	US-09-919-172-55	Sequence 55, Appl1
40	28.4	20.1	335	4	US-09-270-767-2649	Sequence 2649, App
41	28.4	20.1	335	4	US-09-270-767-17931	Sequence 17931, A
42	28.4	20.1	1093	4	US-09-257-179-35	Sequence 35, Appl1
43	28.4	20.1	640681	4	US-09-790-988-1	Sequence 1, Appl1
44	28.4	20.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
45	28.4	20.1	1664976	4	US-09-692-570-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-956-657-1
Sequence 1, Application US/08956657
Patent No. 6210917
GENERAL INFORMATION:
APPLICANT: No. 6210917ori et al., Tautomu
TITLE OF INVENTION: METHOD FOR DETECTION OF
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
NUMBER OF INVENTIONS: CELLS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,342
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/050001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-956-657-1
Query Match 100.0%; Score 141; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 6.8e-33;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
Db 2754 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2813
QY 61 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
Db 2814 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2873
QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2874 TAAAGTAGCATGGCTGCCAG 2894

RESULT 2
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTP) gene
; NAME/KEY: modified base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
US-09-335-231-25

Query Match 100.0%; Score 141; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 6.8e-33;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60

Db 2754 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2813
QY 61 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
Db 2814 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2873
QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2874 TAAAGTAGCATGGCTGCCAG 2894

RESULT 3
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Judas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,413
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD2864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-176-413-1

Query Match 98.9%; Score 139.4; DB 1; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 120
Db 2248 CACTGCTCTCTTCTCTTCAGAAATATGGCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141

Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 4

US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505

; GENERAL INFORMATION:

; APPLICANT: Carrera, Carlos J.
; APPLICANT: Cottam, Howard B.
; APPLICANT: No. 5840505ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
; TITLE OF INVENTION: ACTIVITY IN MALIGNANT METHYLTTHIOADENOSINE PHOSPHORYLASE DEFICI
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,542B
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-612-542B-1

Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTATTAACAACAATCTCAGTAATTACGCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTATTAACAACAATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACCAAGACAT 120
Db 2248 CACTGCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 5
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393

; GENERAL INFORMATION:

; APPLICANT: No. 5942393ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,113
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,855
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD3057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-772-113-1

Query Match 98.9%; Score 139.4; DB 2; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATCAAAATCTGTTTATTAACAACAATCTCAGTAATTACGCCAACATGTGAATAT 60
Db 2188 AATCAAAATCTGTTTATTAACAACAATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACCAAGACAT 120
Db 2248 CACTGCTCTTCTTCTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 6
US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
; GENERAL INFORMATION:
; APPLICANT: No. 6214571ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; APPLICANT: Carrera, Carlos J.

```

; APPLICANT: Coltam, Howard B.
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,137
; FILING DATE: 24-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD3057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-09-199-137-1

Query Match          98.9%; Score 139.4; DB 3; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 60
Db      2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 2247

QY      61 CACTGCTCTTCTTCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
Db      2248 CACTGCTCTTCTTCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307

QY      121 TAAAGTAGCATGGCTGCCAG 141
Db      2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 7
US-08-227-800A-14
; Sequence 14, Application US/08227800A
; Patent No. 6689561
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: NOBORI, TSUTOMU
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
; TITLE OF INVENTION: DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANCER
; TITLE OF INVENTION: TREATMENT
; NUMBER OF SEQUENCES: 18
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,800A
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/023001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: Methylthioadenosine Phosphorylase (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-227-800A-14

Query Match          98.9%; Score 139.4; DB 4; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 60
Db      2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTAGCCCAACATGTGAATAT 2247

QY      61 CACTGCTCTTCTTCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
Db      2248 CACTGCTCTTCTTCTTTCAGATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307

QY      121 TAAAGTAGCATGGCTGCCAG 141
Db      2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 8
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: No. 6689864ori, Tsutomu
; TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
; TITLE OF INVENTION: Detection of Cancer, Monitoring of Tumor Progression and
; TITLE OF INVENTION: Cancer Treatment
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,954
FILING DATE: 26-Aug-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671A
FILING DATE: 18-Jul-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hinesch, Matthew E.
REGISTRATION NUMBER: 47,651
REFERENCE/DOCKET NUMBER: 023070-104042US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..2763
OTHER INFORMATION: /note= "full-length
methylthioadenosine phosphorylase
(MTase) genomic nucleotide sequence"
FEATURE:
NAME/KEY: exon
LOCATION: 254..421
FEATURE:
NAME/KEY: exon
LOCATION: 616..720
FEATURE:
NAME/KEY: exon
LOCATION: 964..1203
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14
Query Match 98.9%; Score 139.4; DB 4; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
DB 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCCTCCTTCTTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
DB 2248 CACTGCCTCCTTCTTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
DB 2308 TAAAGTAGCATGGCTGCCAG 2328
RESULT 9
PCT-US94-14919-1
Sequence 1, Application PC/TUS9414919
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
OF CALIFORNIA
TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
STARVATION OF MALIGNANT CELLS IN MAMMALS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14919
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14919-1
Query Match 98.9%; Score 139.4; DB 5; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
DB 2188 AATCAAAATCTGTTTCTTTTAAACAACATCTCAGTAATTACGCCAACATGTGAATAT 2247
QY 61 CACTGCCTCCTTCTTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
DB 2248 CACTGCCTCCTTCTTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141
DB 2308 TAAAGTAGCATGGCTGCCAG 2328
RESULT 10
PCT-US94-14920-1
Sequence 1, Application PC/TUS9414920
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
OF CALIFORNIA
TITLE OF INVENTION: METHOD FOR DETECTION OF
METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
CELLS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14920
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14920-1
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Query Match          98.9%; Score 139.4; DB 5; Length 2763;
Best Local Similarity 99.3%; Pred. No. 2e-32;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 AATCAAAATCTGTTT TTTT TTTT TTAACAACAATCTCAGTAATTACGCCAATGTGAATAT 60
          |||||
Db       2188 AATCAAAATCTGTTT TTTT TTTT TTAACAACAATCTCAGTAATTACGCCAATGTGAATAT 2247

QY      61 CACTGCCTCTTCTTCTTCTTTCAGAAATATGGCCCAAGTTTCTGTTTATTATCAAGACAT 120
          |||||
Db       2248 CACTGCCTCTTCTTCTTCTTTCAGAAATATGGCCCAAGTTTCTGTTTATTATCAAGACAT 2307

QY      121 TAAAGTAGCATGGCTGCCAG 141
          |||||
Db       2308 TAAAGTAGCATGGCTGCCAG 2328
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RESULT 11
US-09-621-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17307
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17307
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Query Match          42.7%; Score 60.2; DB 4; Length 499;
Best Local Similarity 89.0%; Pred. No. 5e-09;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY      69 CCTTCTTCCTTTCAGAAATATGGCCCAAGTTTCTGTTTATTATCAAGACATTAAGTAG 128
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Db       343 CCTCAATACCTGAAGAATATGGCCCAAGTTTCTGTTTATTATCAAGACATTAAGTAG 402

QY      129 CATGGCTGCCAG 141
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Db       403 CATGGCTGCCAG 415
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RESULT 12
US-09-513-999C-31128
; Sequence 31128, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 31128
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-31128
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Query Match          34.3%; Score 48.4; DB 4; Length 313;
Best Local Similarity 98.0%; Pred. No. 1.4e-05;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db       262 AATCAAAATCTGTTT TTTT TTTT TTAACAACAATCTCAGTAATTACGCCAAC 311
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RESULT 13
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (90001)..(105000)
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LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature

Query Match 23.0%; Score 32.4; DB 4; Length 1230025;
Best Local Similarity 56.6%; Pred. No. 8;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 19 TTTTAACAACATCTCAGTAATTAAGCCACATGTGAATATCACTGCCCTCTTCTTCC 78
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QY 79 TTTCAGATATGCCCCAGTTTCTGTTTATTATTAACAAGACATTAA 124
Db 352231 TTTAATTATTGTCCTTTTGTGATTTCAAAACATAATAATAA 352186

RESULT 14
US-09-335-231-24/C
; Sequence 24, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: anti-sense
; OTHER INFORMATION: primer
US-09-335-231-24

Query Match 22.7%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CCCAGTTTCTGTTTATTATTAACAAGACATTAA 123
Db 32 CCCAGTTTCTGTTTATTATTAACAAGACATTAA 1

RESULT 15
US-08-998-416-302
; Sequence 302, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:

APPLICANT: Phillipsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGCI976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1248UP
US-08-998-416-302

Query Match 21.7%; Score 30.6; DB 3; Length 700;
Best Local Similarity 52.8%; Pred. No. 3.6;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 6 AAATCTGTTTTTTTTTAACAACATCTCAGTAATTAAGCCACATGTGAATATCACTG 65
Db 305 ATACCCGGTGTATTTGATAAAAACTCAGCTCTTCTCTACGCGAGAAATATATATC 364

QY 66 CCTCCTTCTCTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATTAACAAGACATTAAAG 125
Db 365 CAGTCCTTAGCGCCATGCGAAAAATCTGCCCTTTTACCGCTGTTCTCCAGTCTTAGCAC 424

QY 126 TAGCA 130
Db 425 TGGCA 429

Search completed: February 1, 2005, 15:01:01
Job time : 45.1846 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 193.911 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGTTT...AAAGTAGCATGCTGCCAG 141

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	141	100.0	3083	9	US-09-780-114-1
2	141	100.0	3083	15	US-10-326-681-25
3	139.4	98.9	2763	10	US-09-908-671-14
4	61.8	43.8	603	11	US-09-969-034-3235
5	61.4	43.5	1437	15	US-10-106-698-749
6	60.2	42.7	2269	18	US-10-779-476-2
7	54.2	38.4	870	16	US-10-367-366-1
8	38.2	27.1	175561	14	US-10-017-721-3
9	38.2	27.1	175561	16	US-10-235-192A-48
10	34.8	24.7	846	16	US-10-282-122A-11017
11	33.4	23.7	678	13	US-10-027-632-29328
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C 13	33.4	23.7	678	15	US-10-027-632-29328	Sequence 29328, A
C 14	33.4	23.7	678	15	US-10-027-632-29329	Sequence 29329, A
C 15	33.4	23.7	808	13	US-10-027-632-31882	Sequence 31882, A
C 16	33.4	23.7	808	15	US-10-027-632-31882	Sequence 31882, A
C 17	33.4	23.7	107320	13	US-10-087-192-1333	Sequence 1333, Ap
C 18	33.4	23.4	344805	18	US-10-779-271-1	Sequence 1, Appli
C 19	32.6	23.1	111836	17	US-10-322-281-51	Sequence 51, Appl
C 20	32.4	23.0	1230025	16	US-10-289-762-1	Sequence 1, Appli
C 21	32	22.7	32	15	US-10-326-681-24	Sequence 24, Appl
C 22	32	22.7	632	13	US-10-027-632-224812	Sequence 224812,
C 23	32	22.7	632	15	US-10-027-632-224812	Sequence 519, App
C 24	31.6	22.4	56153	16	US-10-221-714A-519	Sequence 25876, A
C 25	31.4	22.3	2106	16	US-10-425-114-25876	Sequence 3145, Ap
C 26	31.2	22.1	1943	9	US-09-938-842A-3145	Sequence 3145, Ap
C 27	31.2	22.1	1943	11	US-09-938-842A-3145	Sequence 4, Appli
C 28	31.2	22.1	161484	17	US-10-317-401-4	Sequence 1, Appli
C 29	31.2	22.1	2731748	17	US-10-297-465A-1	Sequence 26, Appl
C 30	31	22.0	4632	15	US-10-205-219-26	Sequence 924, App
C 31	31	22.0	5173	15	US-10-311-455-924	Sequence 968, App
C 32	30.8	21.8	430	15	US-10-102-524-968	Sequence 81, Appl
C 33	30.8	21.8	430	15	US-10-264-283-81	Sequence 278572,
C 34	30.8	21.8	491	13	US-10-027-632-278572	Sequence 825, App
C 35	30.8	21.8	491	15	US-10-027-632-278572	Sequence 1495, Ap
C 36	30.8	21.8	501	9	US-09-777-564-825	Sequence 825, App
C 37	30.8	21.8	501	9	US-09-777-564-825	Sequence 1495, Ap
C 38	30.8	21.8	501	14	US-10-015-219-825	Sequence 13791, A
C 39	30.8	21.8	501	14	US-10-015-219-1495	Sequence 1, Appli
C 40	30.8	21.8	1984	14	US-10-198-846-13791	Sequence 66, Appl
C 41	30.8	21.8	3641	13	US-10-078-650-1	Sequence 1713, Ap
C 42	30.8	21.8	3641	14	US-10-097-340-66	Sequence 82, Appl
C 43	30.8	21.8	3641	15	US-10-102-524-1713	Sequence 197, App
C 44	30.8	21.8	3641	15	US-10-264-283-82	
C 45	30.8	21.8	5507	18	US-10-473-126-197	

ALIGNMENTS

RESULT 1
US-09-780-114-1
Sequence 1, Application US/09780114
Patent No. US20020146695A1
GENERAL INFORMATION:
APPLICANT: No. US20020146695A1ori, Tsutomu
Carson, Dennis A.
Takabayashi, Kenji
TITLE OF INVENTION: Method for Detection of the Presence or
Absence of Methylthioadenosine Phosphorylase
(MTase) in a
Cell Sample by Detection of the Presence or Absence
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/780,114
FILING DATE: 09-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,914
FILING DATE: 04-May-1998
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/459,343

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; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 08/827,342
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Bastian, Kevin L.
;   REGISTRATION NUMBER: 34,774
;   REFERENCE/DOCKET NUMBER: 023070-103030US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 3083 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 1..3083
;   OTHER INFORMATION: /note= "rat methylthioadenosine
;   phosphorylase (MTase)"
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 119..151
;   OTHER INFORMATION: /note= "exon 1"
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 450..536
;   OTHER INFORMATION: /note= "exon 2"
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 724..782
;   OTHER INFORMATION: /note= "exon 3"
; FEATURE:
;   NAME/KEY: exon
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;   OTHER INFORMATION: /note= "exon 4"
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;   NAME/KEY: exon
;   LOCATION: 1378..1480
;   OTHER INFORMATION: /note= "exon 5"
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;   NAME/KEY: exon
;   LOCATION: 1764..1953
;   OTHER INFORMATION: /note= "exon 6"
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 2426..2548
;   OTHER INFORMATION: /note= "exon 7"
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 2838..2876
;   OTHER INFORMATION: /note= "exon 8"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1
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Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATCAAAATCTGTTT TTTT TTAACAACATCTCAGTAATTACGCCAACATGTGAATAT 60
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QY      61 CACTGCCTCTTCTCTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
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QY      121 TAAAGTAGCATGGCTGCCAG 141
Db      2874 TAAAGTAGCATGGCTGCCAG 2894
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RESULT 2
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
;   APPLICANT: Carson, Dennis A.
;   APPLICANT: Carrera, Carlos J.
;   APPLICANT: Schmidt, Mathias
;   TITLE OF INVENTION: Method for the University of California
;   TITLE OF INVENTION: Prognosis in, Cancer
;   FILE REFERENCE: 023070-108010US
;   CURRENT FILING DATE: 2003-04-15
;   PRIOR APPLICATION NUMBER: US 60/090,411
;   PRIOR FILING DATE: 1998-06-23
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   OTHER INFORMATION: genomic sequence for methylthioadenosine
;   OTHER INFORMATION: phosphorylase (MTAP) gene
; FEATURE:
;   NAME/KEY: modified base
;   LOCATION: (1)..(3083)
;   OTHER INFORMATION: n = unknown
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (119)..(151)
;   OTHER INFORMATION: exon 1
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (450)..(536)
;   OTHER INFORMATION: exon 2
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (724)..(782)
;   OTHER INFORMATION: exon 3
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (899)..(1066)
;   OTHER INFORMATION: exon 4
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1378)..(1480)
;   OTHER INFORMATION: exon 5
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1764)..(1953)
;   OTHER INFORMATION: exon 6
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2426)..(2548)
;   OTHER INFORMATION: exon 7
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2838)..(2876)
;   OTHER INFORMATION: exon 8
US-10-326-681-25
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Query Match      100.0%; Score 141; DB 15; Length 3083;
Best Local Similarity 100.0%; Pred. No. 3e-31;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 CACTGCCTCTTCTCTCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGACAT 120
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Db 2814 CACTGCCTCCTTCTTCTTCAAGATATGCGCCAGTTTCTGTTTATTACCAAGACAT 2873
QY 121 TAAAGTAGCATGGCTGCCAG 141
Db 2874 TAAAGTAGCATGGCTGCCAG 2894

RESULT 3

US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; NOBORI, TSUTOMU
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
TREATMENT
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthiodenosine Phosphorylase (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

Query Match 98.9%; Score 139.4; DB 10; Length 2763;
Best Local Similarity 99.3%; Pred. No. 8.5e-31;
Matches 140; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 2248 CACTGCTCCTTCTTCTTCAAGATATGCGCCAGTTTCTGTTTATTACCAAGACAT 2307
QY 121 TAAAGTAGCATGGCTGCCAG 141

Db 2308 TAAAGTAGCATGGCTGCCAG 2328

RESULT 4

US-09-969-034-3235/c
; Sequence 3235, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3235
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
NAME/KEY: misc feature
LOCATION: 492..497, 506, 527, 542, 544, 573, 576, 597
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235

Query Match 43.8%; Score 61.8; DB 11; Length 603;
Best Local Similarity 96.9%; Pred. No. 3.7e-08;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 77 CCTTCAAGATATGCGCCAGTTTCTGTTTATTACCAAGACATTAAAGTAGCATGGCTG 136
Db 440 CCTTCAAGATATGCGCCAGTTTCTGTTTATTACCAAGACATTAAAGTAGCATGGCTG 381

QY 137 CCCAG 141
Db 380 CCCAG 376

RESULT 5

US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-749

```
Query Match          43.5%; Score 61.4; DB 15; Length 1437;
Best Local Similarity 89.0%; Pred. No. 6.6e-08;
Matches 65; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 69 CCTTCTTCCTTTCAGAAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 128
    ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 104 CCTCCMTAACCTGAAGAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 163

QY 129 CATGGCTGCCAG 141
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 164 CATGGCTGCCAG 176

RESULT 6
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
; APPLICANT: Salmedix, Inc.
; APPLICANT: Leonil, Lorenzo M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
; FILE REFERENCE: 076936-0307942
; CURRENT APPLICATION NUMBER: US/10/779,476
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,888
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/460,715
; PRIOR FILING DATE: 2004-04-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-779-476-2

Query Match          42.7%; Score 60.2; DB 18; Length 2269;
Best Local Similarity 89.0%; Pred. No. 1.8e-07;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 69 CCTTCTTCCTTTCAGAAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 919 CCTCCATAACCTGAAGAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 978

QY 129 CATGGCTGCCAG 141
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 979 CATGGCTGCCAG 991

RESULT 7
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Bei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skallitzky, Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; TITLE OF INVENTION: Phosphorylase Deficient Cells
; FILE REFERENCE: PC19080A (AG110-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
```

```
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

Query Match          38.4%; Score 54.2; DB 16; Length 870;
Best Local Similarity 88.1%; Pred. No. 7.3e-06;
Matches 59; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 69 CCTTCTTCCTTTCAGAAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 804 CCTCCATAACCTGAAGAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAAAGTAG 863

QY 129 CATGGCT 135
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 864 CATGGCT 870

RESULT 8
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Daley, George
; APPLICANT: Bolk, Stacey
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-003
; CURRENT APPLICATION NUMBER: US/10/017,721
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,033
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/330,248
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 175561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-017-721-3

Query Match          27.1%; Score 38.2; DB 14; Length 175561;
Best Local Similarity 58.3%; Pred. No. 2.7;
Matches 67; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 9 TCTGGTTTTTTTTTTAAACAACATCTCAGTAATTAGGCCAACATGTGAATATCACTGCT 68
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3596 TAGGGTTTGTGTTTAAACAACACCTCATCTTTGAATGACTCTGCTGAAACCTAGCAT 3655

QY 69 CCTTCTTCCTTTCAGAAATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAA 123
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3656 TTTTCTTTTTCAGAAATATTCACACTGTATATTAATGAATAAATTGACTAAACATTCA 3710

RESULT 9
US-10-235-192A-48
; Sequence 48, Application US/10235192A
; Publication No. US20040043389A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: Methods and Compositions for Identifying
; TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases
; TITLE OF INVENTION: and Disorders Associated Therewith
; FILE REFERENCE: MMI-011
; CURRENT APPLICATION NUMBER: US/10/235,192A
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 175561
; TYPE: DNA
```



```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329
```

```
Query Match          23.7%; Score 33.4; DB 13; Length 678;
Best Local Similarity 72.9%; Pred. No. 9;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY      60 TCACTGCCTCCTTCTTCTTCCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGAC 118
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      351 TCCCACTGCTGTTTCTTCTTCCTTCAGCCTATGCCCCAGTTTCTGTTTACTGAGAAGGC 293
```

RESULT 13

```
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 29328
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29328
```

```
Query Match          23.7%; Score 33.4; DB 15; Length 678;
Best Local Similarity 72.9%; Pred. No. 9;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY      60 TCACTGCCTCCTTCTTCTTCCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGAC 118
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      351 TCCCACTGCTGTTTCTTCTTCCTTCAGCCTATGCCCCAGTTTCTGTTTACTGAGAAGGC 293
```

RESULT 14

```
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```

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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329
```

```
Query Match          23.7%; Score 33.4; DB 15; Length 678;
Best Local Similarity 72.9%; Pred. No. 9;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY      60 TCACTGCCTCCTTCTTCTTCCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGAC 118
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      351 TCCCACTGCTGTTTCTTCTTCCTTCAGCCTATGCCCCAGTTTCTGTTTACTGAGAAGGC 293
```

RESULT 15

```
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 31882
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-31882
```

```
Query Match          23.7%; Score 33.4; DB 13; Length 808;
Best Local Similarity 72.9%; Pred. No. 9.6;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY      60 TCACTGCCTCCTTCTTCTTCCTTCAGAAATATGCCCCAGTTTCTGTTTATTATACCAAGAC 118
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      351 TCCCACTGCTGTTTCTTCTTCCTTCAGCCTATGCCCCAGTTTCTGTTTACTGAGAAGGC 293
```

Search completed: February 1, 2005, 17:20:31
Job time : 197.911 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 1585.32 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2754_2894
Perfect score: 141
Sequence: 1 AATCAAAATCTGCTTTT...AAAGTAGCATGGTCCAG 141

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	91.4	64.8	687	2	AW976322	AW976322 EST388431
2	61.8	43.8	358	2	BE768971	BE768971 PM4-FT002
3	61.8	43.8	900	5	BX390237	BX390237 BX390237
4	61.2	43.4	370	5	BX495614	BX495614 DKFZp779E
5	60.2	42.7	257	1	AI919501	AI919501 tp22b01.x
6	60.2	42.7	491	1	AA635142	AA635142 af10e10.s
7	60.2	42.7	570	6	CD364939	CD364939 UI-H-FT2-
8	60.2	42.7	612	7	CN409515	CN409515 170006001
9	60.2	42.7	681	4	BM784030	BM784030 K-EST0062
10	60.2	42.7	684	6	CD364946	CD364946 UI-H-FT2-
11	60.2	42.7	819	2	BF981023	BF981023 602310222
12	60.2	42.7	836	1	AL048242	AL048242 DKFZp5860
13	60.2	42.7	836	4	BG574734	BG574734 602596770
14	60.2	42.7	903	5	BX371508	BX371508 BX371508
15	60.2	42.7	911	5	BX350035	BX350035 BX350035
16	60.2	42.7	975	4	BM472910	BM472910 AGENCOURT
17	60.2	42.7	1064	5	BX459089	BX459089 BX459089
18	60.2	42.7	1380	3	BC012316	BC012316 Homo sapi
19	59.8	42.4	1075	1	AL543068	AL543068 AL543068
20	59.4	42.1	401	1	AI674711	AI674711 wd19e10.x
21	57.2	40.6	330	5	BX102948	BX102948 BX102948
22	55	39.0	659	4	BG572739	BG572739 602594259
23	54.6	38.7	388	1	AJ686857	AJ686857 AJ686857
24	53.8	38.2	429	1	AV667881	AV667881 AV667881

25	53.8	38.2	477	4	BG938257	BG938257 1AB014E09
26	53.8	38.2	484	7	CF930825	CF930825 CF--05-R-
27	53.8	38.2	562	4	BI774611	BI774611 466793 MA
28	53.8	38.2	568	7	CO586973	CO586973 DG2-13911
29	53.8	38.2	581	6	CB538214	CB538214 776179 MA
30	53.8	38.2	586	7	CN441464	CN441464 BE04026A1
31	53.8	38.2	600	7	CO701132	CO701132 DG32-195b
32	53.8	38.2	682	7	CN788377	CN788377 4122709 B
33	53.8	38.2	950	7	CF413058	CF413058 CH3#083 G
34	52.8	37.4	609	6	CD535426	CD535426 Leukon5-4
35	51.2	36.3	638	7	CN409513	CN409513 170005327
36	50.6	35.9	729	9	CC543266	CC543266 CH240_424
37	46.6	33.0	755	6	CB946232	CB946232 AGENCOURT
38	46.6	33.0	930	5	BU513490	BU513490 AGENCOURT
39	46.4	32.9	335	2	BE769053	BE769053 PM4-FT002
40	46.4	32.9	1500	3	AK089916	AK089916 Mus muscu
41	46	32.6	1047	4	BM925551	BM925551 AGENCOURT
42	45	31.9	303	6	CA535795	CA535795 C0224810-
43	45	31.9	351	6	CF269885	CF269885 OKST Rat
44	45	31.9	443	6	CA536077	CA536077 C0228H03-
45	45	31.9	529	6	CB545374	CB545374 AMGNNUC:C

ALIGNMENTS

RESULT 1
AW976322/c 687 bp mRNA linear EST 02-JUN-2000
LOCUS AW976322
DEFINITION EST388431 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
ACCESSION AW976322
VERSION AW976322.1 GI:8167548
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 687)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@igr.org
Plate: 359
Seq primer: Forward.
location/Qualifiers
1..687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSkm"
ORIGIN
Query Match 64.8%; Score 91.4; DB 2; Length 687;
Best Local Similarity 98.9%; Pred. No. 6.9e-15;
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATCAAAATCTGTTT...TTTAAACAACATCTCAGTAATTAACGCCACATGTGAATAT 60
DB 101 AATCAAAATCTGTTT...TTTAAACAACATCTCAGTAATTAACGCCACATGTGAATAT 42
QY 61 CACTGCTTCCTTTCTTCTCCTTTCAGAAATATGCCC 93
DB 41 CACTGCTTCCTTTCTTCTCCTTTCAGAAATATGCCC 9

RESULT 2
LOCUS BE768971 358 bp mRNA linear EST 20-SEP-2000
DEFINITION PM4-FT0023-020600-001-d09 FT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE768971
VERSION BE768971.1 GI:10222629
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 358)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=<2=PM4-FT0023-020600-001-d09&tl=2000-06-02&cl=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 358.
Location/Qualifiers
1..358
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="FT0023"
/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source
1..358
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="FT0023"
/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 43.8%; Score 61.8; DB 2; Length 358;
Best Local Similarity 96.9%; Pred. No. 1.1e-06;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 77 CCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATCCAGACATTAAAGTAGCATGGCTG 136
|||
Db 40 CCGTTAAGAAATATGCCCCAGTTTCTGTTTATTATCCAGACATTAAAGTAGCATGGCTG 99
OY 137 CCCAG 141
|||
Db 100 CCCAG 104

RESULT 3
LOCUS BX390237 900 bp mRNA linear EST 28-APR-2004
DEFINITION BX390237 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI002YH04 5-PRIME, mRNA sequence.

ACCESSION BX390237
VERSION BX390237.2 GI:46834877
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30461423.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BAG024ZA09_CS02273_1&c=5445.f

FEATURES
source
1..900
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI002YH04"
/tissue="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 43.8%; Score 61.8; DB 5; Length 900;
Best Local Similarity 90.4%; Pred. No. 1.2e-06;
Matches 66; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 69 CCTTCTCTCCTTTCAGAAATATGCCCCAGTTTCTGTTTATTATCCAGACATTAAAGTAG 128
|||
Db 42 CCTTCCTAACCTGAAGAAATATGCCCCAGTTTCTGTTTATTATCCAGACATTAAAGTAG 101
OY 129 CATGGCTGCCCAG 141
|||
Db 102 CATGGCTGCCCAG 114

RESULT 4
LOCUS BX495614 370 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp779E0622_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
DKFZp779E0622_5', mRNA sequence.

ACCESSION BX495614
VERSION BX495614.1 GI:32010447
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 370)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No RI sequence available. This clone (DKFZp79E0622) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1.370
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp79E0622"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN
Query Match 43.4%; Score 61.2; DB 5; Length 370;
Best Local Similarity 92.5%; Pred. No. 1.6e-06;
Matches 74; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 63 CTGCGCTCTTCTTCCTTCAGATATGCCCACTT-TTCTGTTTATTACCAAGACATT 121
Db 124 CTGCGCTCTTCTTCCTTCAGATATGCCCAAGCTTCTGTTTATTACCAAGCATT 183
QY 122 AAAGTAGCATGGCTGCCAG 141
Db 184 AAAGTNGCNTGGCTGCCAG 203

RESULT 5
AI919501/c 257 bp mRNA linear EST 14-DEC-1999
LOCUS tp22b01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2188489 3'
DEFINITION similar to SW:MTAP_HUMAN Q13126 5'-METHYLTHIOADENOSINE PHOSPHORYLASE ;, mRNA sequence.

ACCESSION AI919501 GI:5639356
VERSION AI919501.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 257)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 246.

FEATURES
source
1..257
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2188489"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"

/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

ORIGIN
Query Match 42.7%; Score 60.2; DB 1; Length 257;
Best Local Similarity 89.0%; Pred. No. 2.8e-06;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 69 CCTTCTCTCTTCAGATATGCCCACTTTCTGTTTATTACCAAGACATTAAAGTAG 128
Db 135 CCTCAATACCTGAAGATATGCCCACTTTCTGTTTATTACCAAGACATTAAAGTAG 76
QY 129 CATGGCTGCCAG 141
Db 75 CATGGCTGCCAG 63

RESULT 6
AA635142/c 491 bp mRNA linear EST 21-OCT-1997
LOCUS af10e10.s1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1031274
DEFINITION 3' similar to TR:G847724 G847724 METHYLTHIOADENOSINE PHOSPHORYLASE.
/; mRNA sequence.

ACCESSION AA635142 GI:2558356
VERSION AA635142.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 491)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 289.

FEATURES
source
1..491
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1031274"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares_testis_NHT"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5',

TGTTACCAATCTGAAGTGGAGCGGCCCAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

BM784030	681 bp	mRNA	linear	EST 05-MAR-2002
LOCUS				
DEFINITION	K-EST0062086 S6SNU620 Homo sapiens CDNA clone S6SNU620-32-F01 5',			
ACCESSION	BM784030			
VERSION	BM784030.1			
KEYWORDS	GI:19132262			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 681)			
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.			
TITLE	21C Frontier Korean EST Project 2001			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 32 row: F column: 01 High quality sequence stop: 681.			
FEATURES	location/Qualifiers			
source	1. 681			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="S6SNU620-32-F01"			
	/sex="F"			
	/tissue_type="Ascites"			
	/cell_type="Scattering floating"			
	/cell_line="SNU-620"			
	/lab_host="Top10F"			
	/clone_lib="S6SNU620"			
	/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."			
ORIGIN				
Query Match	42.7%;	Score 60.2;	DB 4;	Length 681;
Best local Similarity	89.0%;	Pred. No. 3.3e-06;		
Matches	65;	Conservative 0;	Mismatches 8;	Indels 0;
			Gaps 0;	
QY	69 CCTTCTCTCCTTCAGATATGCCCCAGTTTCTGTTTATTACCAAGACATTAAAGTAG	128		
Db	296 CCTCCATAACCTGAAGATATGCCCCAGTTTCTGTTTATTACCAAGACATTAAAGTAG	355		
QY	129 CATGGCTGCCCCAG	141		
Db	356 CATGGCTGCCCCAG	368		
RESULT 10				
LOCUS	CD364946	684 bp	mRNA	linear
DEFINITION	UI-H-FT2-bjn-k-07-0-UI.s1 NCI CGAP FT2 Homo sapiens CDNA clone			EST 05-AUG-2004

ACCESSION	CD364946	UI-H-FT2-bjn-k-07-0-UI 3', mRNA sequence.
VERSION	CD364946.1	GI:31149036
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA=Yes.	
FEATURES	Location/Qualifiers	
source	1. 684	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="UI-H-FT2-bjn-k-07-0-UI"	
	/tissue_type="Alveolar Macrophage"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI_CGAP_FT2"	
	/note="Organ: lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa. TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT2 TAG_SEQ=GGCCATGCCG"	
ORIGIN		
Query Match	42.7%;	Score 60.2; DB 6; Length 684;
Best Local Similarity	89.0%;	Pred. No. 3.3e-06;
Matches	65; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
OY	69 CCTTCTTCCTTCAGATATGCGCCAGTTTCTGTTTATTACCAAGACATTAAAGTAG	128
Db	420 CCTCATTAACCTGAAGAATATGCGCCAGTTTCTGTTTATTACCAAGACATTAAAGTAG	361
OY	129 CATGGCTGCCAG	141
Db	360 CATGGCTGCCAG	348

RESULT	11
LOCUS	BF981023
DEFINITION	602310222F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:440153 5', mRNA sequence.
ACCESSION	BF981023
VERSION	BF981023.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 819)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaphs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM10108 row: k column: 06 High quality sequence stop: 667. location/Qualifiers 1. .819 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4401533" /tissue_type="duodenal adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_88" /note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."
FEATURES	
source	
ORIGIN	
Query Match	42.7%; Score 60.2; DB 2; Length 819;
Best Local Similarity	89.0%; Pred. No. 3.4e-06;
Matches	65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	69 CCTTTCTTCCTTCAGAAATGCCCCAGTTTCTGTATTATTAACAAGCATTAAGTAG 128
Db	99 CTTCCATAAACCCTGAAGAATATGCCCAAGTTTCTGTATTATTAACAAGCATTAAGTAG 158
OY	129 CATGGCTGCCCGAG 141
Db	159 CATGGCTGCCCGAG 171
RESULT	12
LOCUS	AL048242 836 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKEZP586O1023_r1 586 (synonym: hutel) Homo sapiens cDNA clone DKEZP586O1023, mRNA sequence.
ACCESSION	AL048242
VERSION	AL048242.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 836)
TITLE	Ansorge,W., Winkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S. EST (Ansorge, et al.)

```
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
             MIPS
             Ingolstaedter landstr.1, D-85764 Neuherberg, Germany
             This is the 5' sequence of the clone insert
             Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
             Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
             sequenced by EMBL (European Molecular Biology Laboratories,
             Heidelberg/Germany) within the cDNA sequencing consortium of the
             German Genome Project.
             No sl sequence available.
             This clone (DKFP58601023) is available at the RZPD in Berlin.
             Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
             Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES     Location/Qualifiers
source       1..836
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="DKFP58601023"
             /tissue_type="uterus"
             /dev_stage="adult"
             /lab_host="DH10B"
             /clone_lib="586 (synonym: hutel)"
             /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
ORIGIN
Query Match          42.7%; Score 60.2; DB 1; Length 836;
Best Local Similarity 89.0%; Pred. No. 3.4e-06;
Matches 65; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY               69 CCTTCTTCCTTCAGATATGGCCCGAGTTTCTGTTATTATACCAAGACATTAAAGTAG 128
                  ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB               305 CCTCATTAACCTGAAGAATATGGCCAGTTTCTGTTATTATACCAAGACATTAAAGTAG 364
OY               129 CATGGCTGCCCAG 141
                  ||||| | | | | | | | | | | | | | | | | | | | | | | | |
DB               365 CATGGCTGCCCAG 377
RESULT 13
BG574734              836 bp mRNA linear EST 10-APR-2001
BG574734 LOCUS
DEFINITION   BG574734.1 GI:13582387 Homo sapiens CDNA clone IMAGE:4705673 5',
              mRNA sequence.
ACCESSION   BG574734
VERSION     BG574734.1
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 836)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LINL at:
            http://image.llnl.gov
            Plate: LHAM10572 row: k column: 18
            High quality sequence stop: 680.
FEATURES     Location/Qualifiers
source       1..836
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:4705673"
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```

/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/notes="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match	42.7%	Score 60.2;	DB 4;	Length 836;
Best Local Similarity	89.0%;	Pred. No. 3.4e-06;		
Matches 65; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

Oy 69 CCTTCTCTCCTTCAGAAATATGCCACGTTTCTGTATTATTAACAAGACATTAAAGTAG 128
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 CCTCCATAACCTGAAGAATATGGCCACGTTTCTGTATTATTAACAAGACATTAAAGTAG 65

Oy	129	CATGCTGCCAG	141
Db	66	CATGCTGCCAG	78

RESULT 14
BX371508/

LOCUS	903 bp	mRNA	linear	EST 26-APR-2004
DEFINITION	BX371508			
	BX371508	Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens	CDNA
	clone CS0D1002YH04	3-PRIME, mRNA		sequence.

ACCESSION	BX371508
VERSION	BX371508.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 903)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope

Genoscope - Centre National de Séquencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5445.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0BA1016ZHO7> CS01496 1&c=5445.f

FEATURES	Location/Qualifiers
Source	1. .903

```

Location/Qualifiers
1. .903
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI002YH04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1fb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/primer="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

ORIGIN

Query Match	42.7%	Score 60.2;	DB 5;	Length 903;
Best Local Similarity	89.0%;	Pred. No. 3.4e-06;		
Matches 65; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

Oy 69 CCTTCTCCTTCAGATATGGCCAGTTTCTGTTTATTACCAAGACAATAAAGTAG 128
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 616 CTTCCATAACCCTGAAGAATATGGCCAGTTTCTGTTTATTACCAAGACATTAAAGTAG 557

QY	129	CATGGCTGCCAG	141
Db	556	CATGGCTGCCAG	544

RESULT 15
BX350035/c

LOCUS	911 bp	mRNA	linear	EST 08-APR-2004
DEFINITION	BX350035	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI002YH06 3-PRIME, mRNA sequence.		

KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 911)
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)

COMMENT

On May 5, 2003 this sequence version replaced gi:30377483.
Contact: Genoscope
Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
340.r
There is a virtual cDNA representing this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdna?c=CS0BA1016ZB08_CS01498_2&c=340.r.

FEATURES

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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

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Best Local Similarity	89.0%;	Pred. No. 3.4e-06;		
Matches 65; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY	129	CATGGCTGCCAG	141
Db	549	CATGGCTGCCAG	537

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Job time : 1589.32 secs

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Job time : 1589.32 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 219.128 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876

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Sequence: 1 AATATGCCCGAGTTTCTGTTTATTATCCAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	39	100.0	383	9	AH013410S8	L42634 Homo sapien
2	39	100.0	499	6	AR425810	AR425810 Sequence
3	39	100.0	499	6	AX986504	AX986504 Sequence
4	39	100.0	499	6	BD121363	BD121363 EST and e
5	39	100.0	852	9	CR541670	CR541670 Homo sapi
6	39	100.0	870	6	AX826996	AX826996 Sequence
7	39	100.0	1021	9	L40432	L40432 Homo sapien
8	39	100.0	1890	9	BC026106	BC026106 Homo sapi
9	39	100.0	2269	9	HSU22233	U22233 Human methy
10	39	100.0	2763	6	AR059583	AR059583 Sequence
11	39	100.0	2763	6	I28320	I28320 Sequence 1
12	39	100.0	2763	6	AR473576	AR473576 Sequence
13	39	100.0	2763	6	AR474046	AR474046 Sequence
14	39	100.0	3083	6	AR144466	AR144466 Sequence
15	39	100.0	3083	6	AR342446	AR342446 Sequence
16	39	100.0	168656	9	AL359922	AL359922 Human DNA
17	39	100.0	250000	9	AB060808	AB060808 Homo sapi
18	36	92.3	849	9	CR541710	CR541710 Homo sapi
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20	32.6	83.6	2565	10	BC003858	BC003858 Mus muscu
21	32.6	83.6	194025	10	AL831719	AL831719 Mouse DNA
22	32.6	83.6	225782	2	AC109529	AC109529 Rattus no
23	32.6	83.6	287775	2	AC108638	AC108638 Rattus no
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25	24.8	63.6	212886	2	AC093946	AC093946 Rattus no
26	24.8	63.6	234471	2	AC121424	AC121424 Rattus no
27	24.6	63.1	122176	2	AL358233	AL358233 Homo sapi
28	24.6	63.1	152224	2	AC007933	AC007933 Homo sapi
29	24.6	63.1	155046	2	CR450771	CR450771 Danio rer
30	24.6	63.1	175046	2	AC022728	AC022728 Homo sapi
31	24.6	63.1	188983	2	BX511222	BX511222 Danio rer
32	24.6	63.1	193774	9	AL445183	AL445183 Human DNA
33	24.6	63.1	232296	2	CR392026	CR392026 Danio rer
34	24.4	62.6	40011	9	AC026364	AC026364 Homo sapi
35	24.4	62.6	177594	9	AC026368	AC026368 Homo sapi
36	24.4	62.6	194919	2	AC127899	AC127899 Homo sapi
37	24.2	62.1	221189	2	AC131130	AC131130 Rattus no
38	24.2	62.1	228972	2	AC139930	AC139930 Rattus no
39	24.2	62.1	233619	2	AC128426	AC128426 Rattus no
40	24.2	62.1	248032	2	AC105801	AC105801 Rattus no
41	24.2	62.1	250876	2	AC097179	AC097179 Rattus no
42	24.2	62.1	324359	2	AC127115	AC127115 Rattus no
43	24	61.5	117406	9	AC010792	AC010792 Homo sapi
44	24	61.5	177152	9	BX544879	BX544879 Human DNA
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ALIGNMENTS

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LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SEGMENT					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
PUBMED					
FEATURES					
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Best Local Similarity	100.0%;	Pred. No. 0.00068;		
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Qy	1	AATATGGCCAGTTTCTGTATTATTAACCAAGACATTAA	39
Db	138	AATATGCCCCAGTTTTCTGTATTATTAACCAAGACATTAA	176

RESULT 2				
AR425810				PAT 18-DEC-2003
LOCUS	AR425810	499 bp	DNA	linear
DEFINITION	Sequence	17307 from patent US 6639063.		
ACCESSION	AR425810			
VERSION	AR425810.1	GI:40180920		

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 499)
TITLE	Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
JOURNAL	EST's and encoded human proteins
FEATURES	Patent: US 6639063-A 17307 28-OCT-2003;
	Location/Qualifiers
source	1. .499

ORIGIN

Query Match	100.0%;	Score 39;	DB 6;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 0.00065;		
Matches 39;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 359 AATATGCCCGAGTTTCTGTTTTATTACCAAGACATTAA 397

RESULT 3			
AX986504			
LOCUS	AX986504	499 bp	DNA
DEFINITION	Sequence 17307	from Patent EP1104808.	linear
ACCESSION	AX986504		PAT 15-JAN-2004
VERSION	AX986504.1	GI:40992644	

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	AUTHORS
1	Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.

JOURNAL Patent: EP 1104808-A 17307 06-JUN-2001;

Location/Qualifiers

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RESULT 4
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BDI21363	499 bp	DNA	linear	PAT 18-SEP-2002
EST and encoded human protein.				
DEFINITION				
LOCUS				

ACCESSION BD121363
VERSION BD121363.1 GI:23216273
KEYWORDS JP 2002010789-A/13440.

ORGANISM	Homo sapiens
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REFERENCE 1 (bases 1 to 499)

AUTHORS Edwards, J.B.D.M., Jobert, S., and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 13440 15-JAN-2002;

COMMENT

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/13440

PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21, PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC

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FEATURES

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URRES
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Location/Qualifiers
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Qy 1 AATATGCCCAGTTTCTGTTTATTACCAAGACATTAA 39
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Db 359 AATATGCCCAGTTTCTGTTTATTACCAAGACATTAA 397

RESULT 5
CR541670

LOCUS	CR541670	852 bp	mRNA	linear	PRI 29-JUN-2004
DEFINITION	Homo sapiens full open reading frame cDNA clone RZPD08343127D for				

stopcodon.

ACCESSION	CR541670	GI:49456300
VERSION	CR541670.1	

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens


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RESULT 8
BC026106

LOCUS BC026106 1890 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone

MGC:33067 IMAGE:4820938), complete cds.

ACCESSION BC026106
VERSION BC026106.1 GI:19913486
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1890)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettaman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE human and initial analysis of more than 15,000 full-length
house and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE PUBMED 12477932

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (26-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettaman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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gene

CDS

ORIGIN

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RESULT 9
HSU22233

LOCUS HSU22233 2269 bp mRNA linear PRI 25-NOV-1995
DEFINITION Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.

ACCESSION U22233

VERSION U22233.1 GI:847723

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2269)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Olopade,O.I., Pomyskala,H.M., Hagos,F., Sveen,L.W., Espinosa,R. III,
Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and
Bohlender,S.K.

TITLE Construction of a 2.8-megabase yeast artificial chromosome contig

and cloning of the human methylthioadenosine phosphorylase gene
from the tumor suppressor region on 9p21
Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)

JOURNAL MEDLINE
PUBMED 95327672
REFERENCE 2 (bases 1 to 2269)
AUTHORS Olopade,O.I.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,
University of Chicago Pritzker School of Medicine, 5841 S. Maryland
Avenue, Chicago, IL 60637-1470, USA

FEATURES
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QY 1 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 39
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Db 935 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 973

RESULT 10
AR059583 2763 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 1 from patent US 5840505.
ACCESSION AR059583
VERSION AR059583.1 GI:5986033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2763)
AUTHORS Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
TITLE Method for inhibiting adenylosuccinate synthetase activity in
methylthioadenosine phosphorylase deficient cells
JOURNAL Patent: US 5840505-A 1 24-NOV-1998;
FEATURES location/Qualifiers
SOURCE 1..2763
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 39; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 39
|||||
Db 2272 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 2310

RESULT 11
128320 2763 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 1 from patent US 5571510.
ACCESSION 128320
VERSION 128320.1 GI:1819096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unclassified.
1 (bases 1 to 2763)
AUTHORS Nobori,T. and Carson,D.A.
TITLE Method for selective methionine starvation of malignant cells in
mammals

JOURNAL Patent: US 5571510-A 1 05-NOV-1996;
FEATURES location/Qualifiers
SOURCE 1..2763
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 39; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 39
|||||
Db 2272 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 2310

RESULT 12
AR473576 2763 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 14 from patent US 6689561.
ACCESSION AR473576
VERSION AR473576.1 GI:42711901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2763)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Tumor suppressor gene and methods for detection of cancer,
monitoring of tumor progression and cancer treatment
JOURNAL Patent: US 6689561-A 14 10-FEB-2004;
FEATURES location/Qualifiers
SOURCE 1..2763
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 39; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 39
|||||
Db 2272 AATATGCCCCAGTTTCTGTTTATTATCAAGACATTAA 2310

RESULT 13
AR474046 2763 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 14 from patent US 6689864.
ACCESSION AR474046
VERSION AR474046.1 GI:42712799
KEYWORDS
SOURCE Unknown.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 51.1826 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876

Perfect score: 39
Sequence: 1 AATATGCCCGAGTTTCTGTTTATTAACCAAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	39	100.0	603	6	ABQ59540	Abq59540 Human col
2	39	100.0	870	10	ADC37133	Adc37133 Cloned me
3	39	100.0	1437	4	AAH33683	Aah33683 Human col
4	39	100.0	2197	10	ADC30327	Adc30327 Human nov
5	39	100.0	2763	2	AAT15167	Aat15167 Methy1thi
6	39	100.0	2763	2	AAQ92813	Aaq92813 Human MTA
7	39	100.0	2763	2	AAT85305	Aat85305 Human met
8	39	100.0	2763	2	AAZ00866	Aaz00866 Human MTA
9	39	100.0	2763	5	AAF86091	Aaf86091 Methy1thi
10	39	100.0	2763	10	AAD64097	Aad64097 Human met
11	39	100.0	2784	2	AAQ99202	Aaq99202 Pseudomon
12	39	100.0	3083	2	AAK58284	Aax58284 Human met
13	39	100.0	3083	8	ABX10818	Abx10818 DNA encod
C 14	32	82.1	32	3	AAZ35375	Aaz35375 Methy1thi
C 15	23	59.0	554	6	ABN87814	Abn87814 Human ova
C 16	23	59.0	554	8	ABX92240	Abx92240 Human ova
C 17	22.6	57.9	168575	4	AAH21613	Aah21613 Human hyp
18	22	56.4	22	3	AAZ35354	Aaz35354 Sense pri
C 19	21.8	55.9	110000	6	ABA90521_05	Continuation (6 of
20	21.6	55.4	302250	6	ABL67703	Ab167703 Oesophagu
21	21.4	54.9	577	10	ADF74440	Adf74440 Murine ma

C	22	21.4	54.9	1062	6	ABZ13834	Abz13834 Arabidops
	23	21.4	54.9	1107	2	AAT76896	Aat76896 Brassica
	24	21.4	54.9	1120	2	AAV58304	Aav58304 Brassica
	25	21.4	54.9	1120	3	AAC61419	Aac61419 Genomic D
	26	21.4	54.9	1389	10	ADF18054	Adf18054 Mouse mat
C	27	21.4	54.9	1390	10	ADB31856	Adb31856 DNA encod
C	28	21.4	54.9	1390	12	ADO02262	Ado02262 Thalecres
C	29	21.4	54.9	1484	3	AAC47412	Aac47412 Arabidops
C	30	21.4	54.9	1487	3	AAC36225	Aac36225 Arabidops
	31	21.4	54.9	1790	10	ADF18052	Adf18052 CDNA encd
	32	21.4	54.9	1790	10	ADF74446	Adf74446 Full leng
	33	21.4	54.9	1790	12	ADI53689	Adi53689 Murine ma
	34	21.4	54.9	2421	2	AAT30867	Aat30867 80 kD pro
	35	21.4	54.9	2421	2	AAT85373	Aat85373 Tetrahyme
	36	21.4	54.9	2746	11	ADM03683	Adm03683 Human CDN
	37	21.4	54.9	3559	11	ADM01917	Adm01917 Human CDN
	38	21.4	54.9	9881	6	AB154354	Ab154354 Chemical1
	39	21.4	54.9	11847	4	ABL29442	Ab129442 Drosophil
	40	21.4	54.9	11847	4	AAE57196	Aae57196 DNA encod
	41	21.4	54.9	11847	10	ADC35935	Adc35935 Drosophil
C	42	21.4	54.9	13427	6	ABL33927	Ab133927 Human.imm
	43	21.4	54.9	18817	6	ABL34494	Ab134494 Human met
	44	21.4	54.9	18817	6	ABL70161	Ab170161 Chemical1
	45	21.4	54.9	60940	9	ADA02582	Ada02582 Human REL

ALIGNMENTS

RESULT 1	ABQ59540/c
ID	ABQ59540 standard; cDNA; 603 BP.
XX	
AC	ABQ59540;
XX	
DT	02-AUG-2002 (first entry)
XX	
DE	Human colon cancer related nucleotide sequence SEQ ID NO:3235.
XX	
KW	Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW	genetic analysis; diagnostic; antisense therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200229086-A2.
XX	
PD	11-APR-2002.
XX	
PF	02-OCT-2001; 2001WO-US030732.
XX	
PR	02-OCT-2000; 2000US-0237271P.
XX	
PA	(FARB) BAYER CORP.
XX	
PI	Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI	Thiaglingam A, Lewis ME;
XX	
DR	WPI; 2002-426115/45.
XX	
PT	New isolated nucleic acid that is differentially expressed in cancer
PT	tissues useful for determining the presence of colon cancer in a cell or
PT	tissue type, and in antisense therapy.
XX	
PS	Claim 1; Fig 1; 796pp; English.
XX	
CC	ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC	expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC	encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC	used in antisense therapy. An antibody immunoreactive with a polypeptide
CC	encoded by (I) is useful for detecting cancer in a patient sample, and
CC	for detecting the presence or absence of a polynucleotide encoded by a
CC	nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC	from (I) can be used for determining the presence of a nucleic acid which

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTTTATTATCCAGACATTAA 39
Db 120 AATATGCCCGAGTTTCTGTTTATTATCCAGACATTAA 158

RESULT 4
ID ADC30327 standard; cDNA; 2197 BP.

AC ADC30327;

DT 18-DEC-2003 (first entry)

DE Human novel cDNA sequence, SEQ ID NO:409.

KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antilucer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 3; gene; ss.

OS Homo sapiens.

PN WO2003029271-A2.

PD 10-APR-2003.

PF 24-SEP-2002; 2002WO-US030474.

PR 24-SEP-2001; 2001US-0324631P.

PA (HYSE-) HYSEQ INC.

PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;

PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;

PI Haley-Vicente D, Drmanac RT;

DR WPI; 2003-371981/35.

DR P-PSDB; ADC31298.

XX New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.

XX Claim 1; SEQ ID NO 409; 1185pp; English.

XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition, kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are

CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 10; Length 2197;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTTTATTATCCAGACATTAA 39
Db 874 AATATGCCCGAGTTTCTGTTTATTATCCAGACATTAA 912

RESULT 5
ID AAT15167 standard; DNA; 2763 BP.

AC AAT15167;

DT 29-JUN-1996 (first entry)

DE Methylthioadenosine-phosphorylase gene.

KW Human; methylthioadenosine-phosphorylase; chromosome walking;
KW interferon-alpha; CDK41; tumour suppressor; chromosome-9p21;
KW cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW antibody; imaging; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT exon 254.. .421

FT intron /*tag= b

FT exon /*tag= c

FT exon 616.. .720

FT intron /*tag= d

FT exon 721.. .963

FT exon /*tag= e

FT exon 964.. .1203

FT exon /*tag= f

PN WO9528169-A1.

PD 26-OCT-1995.

PF 12-APR-1995; 95WO-US004655.

PR 14-APR-1994; 94US-00227800.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Nobori T;

DR WPI; 1995-373630/48.

XX Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT useful for diagnosis, assessing predisposition and treatment of cancers.
XX Example 1; Page 96-101; 129pp; English.

CC The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK41)
CC tumour suppressor gene (AAT15157-58) is located between this gene and an
CC interferon-alpha gene cluster, and has been isolated by chromosome
CC walking. The CDK41 gene, probe and primer derivatives and the gene
CC product may be used in diagnosis of cancer, particularly melanoma
CC (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC or in antitumour antisense oligonucleotide or ribozyme construction.
CC Antibodies against CDK41 may be used in diagnosis or in vivo imaging
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 2272 AATATGCCCCAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 6
AAQ92813
ID AAQ92813 standard; DNA; 2763 BP.
XX
AC AAQ92813;
XX
DT 25-MAR-2003 (revised)
DT 05-DEC-1995 (first entry)
XX
DE Human MTase.
XX
KW MTase; methyladenosine-phosphatase; malignancy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254..421
FT exon /*tag= a
FT exon 616..720
FT exon /*tag= b
FT exon 964..1203
FT exon /*tag= c
FT exon 1640..1762
FT exon /*tag= d
FT exon 2272..2310
FT exon /*tag= e
XX
XX
PN WO9518233-A1.
XX
PD 06-JUL-1995.
XX
PF 22-DEC-1994; 94WO-US014920.
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
PA (CIBA) CIBA GEIGY CORP.
XX
PI Nobori T, Carson DA, Takabayashi K;
XX
DR WPI; 1995-246398/32.
XX
PT Detecting methyladenosine phosphatase in mammalian cells - by
PT hybridisation with specific oligonucleotide for detecting malignancy,
PT also new nucleic acid, expression vectors, derived polypeptide(s) and
PT antibodies.
XX
PS Claim 8; Page 34-35; 47pp; English.
XX
CC A cosmid gene library constructed from human placenta DNA was screened
CC using a MTase cDNA probe to isolate a human MTase genomic clone (sequence

CC given in AAQ92813). Absence of MTase from a cell is indicative of
CC malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 2272 AATATGCCCCAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 7
AAT85305
ID AAT85305 standard; DNA; 2763 BP.
XX
AC AAT85305;
XX
DT 28-FEB-1998 (first entry)
XX
DE Human methylthioadenosine phosphorylase.
XX
KW Methylthioadenosine phosphorylase; MTase; human;
KW adenylosuccinate synthetase; lung cancer; glioma;
KW acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254..421
FT exon /*tag= a
FT intron /number= 1
FT intron 422..615
FT intron /*tag= b
FT intron /number= 1
FT exon 616..720
FT exon /*tag= c
FT intron /number= 2
FT intron 721..963
FT intron /*tag= d
FT intron /number= 2
FT exon 964..1203
FT exon /*tag= e
FT exon /number= 3
XX
XX
PN WO9732994-A1.
XX
PD 12-SEP-1997.
XX
PF 27-JAN-1997; 97WO-US001193.
XX
PR 08-MAR-1996; 96US-00612542.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carrera CU, Carson DA, Cottam HB, Nobori T;
XX
DR WPI; 1997-470550/43.
XX
PT Inhibiting adenylosuccinate synthetase activity in methylthio:adenosine
PT phosphorylase-deficient cells - by treatment with specific inhibitor,
PT especially L-alanosine, useful for selective killing of MTase deficient
PT cancer cells.
XX
PS Example 3; Page 25-26; 37pp; English.
XX
CC This DNA sequence comprises human genomic DNA for methylthioadenosine
CC phosphorylase (MTase), obtained from a cosmid gene library constructed
CC from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC method for inhibiting the activity adenylosuccinate synthetase (Ass) in
CC mammalian cells deficient in MTase activity involves: (a) determining

CC that a population of cells obtained from a mammalian host is MTase
CC deficient; and (b) administering an ASS inhibitor (preferably L-
CC alanosine) to the host so that the MTase deficient host cells are
CC depleted of AMP. The method is especially used to treat human MTase-
CC deficient primary tumour cells, specifically non-small cell lung cancer,
CC acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC MTase catabolises methylthioadenosine to adenine for endogenous salvage
CC incorporation into the intracellular AMP pool. The claimed method
CC deprives the cells of substrate for de novo synthesis of AMP, resulting
CC in selective killing of these cells. MTase sequence-specific
CC oligonucleotides can be used to detect the presence or absence of MTase in
CC malignant cell lines
XX
SQ Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39
|||
Db 2272 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 2310

RESULT 8
AAZ00866
ID AAZ00866 standard; DNA; 2763 BP.
XX
AC AAZ00866;
XX
DT 20-OCT-1999 (first entry)
XX
DE Human MTase DNA.
XX
KW MTase; methylthioadenosine phosphorylase; human; detection; active;
KW catalytic; malignant cell; methionine starvation therapy; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT exon 253..421
FT /*tag= a
FT /number= 1
FT /note= "Putative exon"
FT 422..615
FT /*tag= b
FT /number= 1
FT /note= "putative intron"
FT 616..720
FT /*tag= c
FT /number= 2
FT /note= "putative exon"
FT 721..963
FT /*tag= d
FT /number= 2
FT /note= "putative intron"
FT 964..1203
FT /*tag= e
FT /number= 3
FT /note= "putative exon"
XX
XX
PN US5942393-A.
XX
PD 24-AUG-1999.
XX
XX
PF 18-DEC-1996; 96US-00772113.
XX
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Takabayashi K, Carson DA, Nobori T;
XX

DR WPI; 1999-507775/42.
XX
XX
PT Detecting catalytically active and inactive methylthioadenosine
PT phosphorylase (MTase) in mammalian cells useful for identifying malignant
PT cells which are suitable targets for methionine (MET) starvation therapy;
XX
PS Claim 6; Fig 1; 14pp; English.
XX
XX This invention describes a novel method for detecting catalytically
CC active and inactive methylthioadenosine phosphorylase (MTase) in
CC mammalian cells, using oligonucleotide probes which hybridize to MTase
CC nucleic acid coding regions. Detection of MTase encoding nucleic acid
CC indicates the cell has catalytically active MTase. The method is useful
CC for detecting malignant cells with a deficient MTase gene, useful for
CC identifying malignant cells which are suitable targets for methionine
CC (MET) starvation therapy. The new method is simple, efficient and
CC successful at determining MTase negative cells, unlike prior art
CC techniques, which include analysis of catalytic activity in cell
CC cultures, requiring a commercially unavailable radiochemical substrate,
CC and immunoassays, using MTase antibodies which are unable to be produced
CC in sufficient quantities. Recombinant MTase protein produced using the
CC new polynucleotide and vector, allows greater and purer production of
CC MTase than prior art techniques (using the Rangione method) for isolating
CC native MTase. This sequence represents human MTase encoding DNA which is
CC used in the method of the invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39
|||
Db 2272 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 2310

RESULT 9
AAF86091
ID AAF86091 standard; DNA; 2763 BP.
XX
AC AAF86091;
XX
DT 06-JUL-2001 (first entry)
XX
DE Methylthioadenosine phosphorylase.
XX
DE Methylthioadenosine phosphorylase.
XX
KW Methylthioadenosine phosphorylase; adenyly succinate synthetase; ASS;
KW cancer; ds.
XX
XX
OS Unidentified.
XX
XX
PN US6214571-B1.
XX
XX
PD 10-APR-2001.
XX
XX
PF 24-NOV-1998; 98US-00199137.
XX
XX
PR 29-DEC-1993; 93US-00176855.
XX
XX
PA (REGC) UNIV CALIFORNIA.
XX
XX
PI Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
XX WPI; 2001-315458/33.
XX
XX
XX Inhibiting adenine succinate synthetase (ASS) activity in
PT methylthioadenosine phosphorylase deficient cells of mammalian host
PT involves administering ASS inhibitor which depletes adenosine 5'
PT monophosphate in cells.
XX
XX
PS Disclosure; Fig 1; 17pp; English.
XX

CC The present invention relates to inhibiting adeny1 succinate synthetase
CC (ASS) activity in methylthioadenosine phosphorylase (MTase) deficient
CC cells of mammalian host. The invention may be used as a treatment for
CC cancer, especially breast and colon cancer

XX
SQ Sequence 2763 BP, 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 39
|||
Db 2272 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 10
AAD64097
ID AAD64097 standard; DNA; 2763 BP.

XX AAD64097;

XX 12-FEB-2004 (first entry)

DE Human methylthioadenosine phosphorylase (MTase) genomic DNA.

XX
KW Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTase;
KW ds.

XX
OS Homo sapiens.

FH Key Location/Qualifiers

FT exon 254..421
/*tag= a
FT intron 422..615
/*tag= b
FT exon 616..720
/*tag= c
FT intron 721..963
/*tag= d
FT exon 964..1203
/*tag= e

XX US2003138928-A1.

XX 24-JUL-2003.

XX 18-JUL-2001; 2001US-00908671.

XX 26-AUG-1997; 97US-00921954.

XX (CARs/) CARSON D A.
XX (NOBO/) NOBORI T.

XX Carson DA, Nobori T;

XX WPI; 2003-851737/79.

XX
PT New isolated polynucleotide encoding cyclin-dependent kinase 4I, useful
PT for preparing a composition for diagnosing or treating cancer.

XX
PS Example 1; SEQ ID NO 14; 46pp; English.

XX The present invention relates to novel tumour suppressor genes, termed as
CC cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC proteins. The polynucleotides are useful for preparing a composition for
CC diagnosing or treating cancer. Sequences of the invention are also useful
CC in gene therapy. The present sequence is human methylthioadenosine
CC phosphorylase (MTase) genomic DNA used in the exemplification of the
CC invention

XX
SQ Sequence 2763 BP, 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 39; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 39
|||
Db 2272 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 11
AAQ99202
ID AAQ99202 standard; DNA; 2784 BP.

XX AAQ99202;

XX 07-MAR-1996 (first entry)

DE Pseudomonas putida methylthioadenosine-phosphorylase DNA.

XX
KW Enzyme; MTase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW chemotherapy; cancer therapy; methionine starvation; ss.

XX
OS Pseudomonas putida.

FH Key Location/Qualifiers

FT CDS 1..2763
/*tag= a

XX WO9517908-A1.

XX 06-JUL-1995.

XX 22-DEC-1994; 94WO-US014919.

XX 29-DEC-1993; 93US-00176413.

XX (REGC) UNIV CALIFORNIA.

XX Nobori T, Carson DA;

XX WPI; 1995-246192/32.

XX
PT Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT negative tumour cells - used in chemotherapy of mammalian malignant
PT cells.

XX
PS Disclosure; Page 27-28; 46pp; English.

XX
CC Antigenic peptides may be generated from this sequence encoding
CC methyladenosine-phosphorylase, which are then used to generate antibodies
CC specific for MTase. The produced antibodies may be used in an immunoassay
CC for the detection of MTase

XX
SQ Sequence 2784 BP, 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

Query Match 100.0%; Score 39; DB 2; Length 2784;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 39
|||
Db 2272 AATATGCCCGAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 12
AA58284
ID AA58284 standard; DNA; 3083 BP.

XX AA58284;

XX 02-AUG-1999 (first entry)

XX

DE	Human methylthioadenosine phosphorylase genomic DNA.	
XX		
KW	Methylthioadenosine phosphorylase; MTase; human;	
KW	multiple drug resistance; multidrug resistance; cancer; leukaemia;	
XX	therapy; ss.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	119..2876
FT		/*tag= a
FT	exon	/note= "contains introns"
FT		119..151
FT		/*tag= b
FT	intron	/number= 1
FT		152..449
FT		/*tag= c
FT	exon	/number= 1
FT		450..536
FT		/*tag= d
FT	intron	/number= 2
FT		537..723
FT		/*tag= e
FT	exon	/number= 2
FT		724..782
FT		/*tag= f
FT	intron	/number= 3
FT		783..898
FT		/*tag= g
FT	exon	/number= 3
FT		899..1067
FT		/*tag= h
FT	intron	/number= 4
FT		1068..1377
FT		/*tag= i
FT	exon	/number= 4
FT		1378..1480
FT		/*tag= j
FT	intron	/number= 5
FT		1481..1763
FT		/*tag= k
FT	exon	/number= 5
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FT	intron	/number= 6
FT		1954..2425
FT		/*tag= m
FT	exon	/number= 6
FT		2426..2548
FT		/*tag= n
FT	intron	/number= 7
FT		2549..2837
FT		/*tag= o
FT	exon	/number= 7
FT		2838..2876
FT		/*tag= p
FT		/number= 8
XX		
PN	WO9920791-A1.	
XX		
PD	29-APR-1999.	
XX		
PF	23-OCT-1998;	98WO-US022557.
XX		
PR	23-OCT-1997;	97US-00956657.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Carson DA, Cottam HB, Nobori T, Carrera CJ;	
XX		
DR	WPI; 1999-302753/25.	
XX		
PT	Suppression of multiple drug resistance in cells, for treatment of, e.g.	

PT	leukemia's.	
XX		
PS	Example 3; Page 42-44; 45pp; English.	
XX		
CC	This is the DNA sequence of a human methylthioadenosine phosphorylase	
CC	(MTase) genomic DNA clone that was isolated from a cosmid gene library	
CC	using an MTase cDNA probe. The encoded enzyme catabolises	
CC	methylthioadenosine to adenine for endogenous salvage incorporation into	
CC	the intracellular AMP pool. The invention relates to methods for treating	
CC	and preventing the onset and maintenance of multiple drug resistance	
CC	(MDR) in animals undergoing cancer chemotherapy. In the methods provided,	
CC	cells are depleted of AMP and ATP and are thus unable to supprt P-	
CC	glycoprotein activity. One method obtains a population of target cells	
CC	from a host and assays for loss of MTase activity. MTase deficient cells	
CC	are treated with a purine synthesis inhibitor, such as L-alanosine, which	
CC	starves the cells of adenine and suppresses P-glycoprotein activity. The	
CC	MTase deficient host cells are preferably primary tumour cells comprising	
CC	small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma	
CC	cells or urothelial tumor cells, preferably in humans. MTase competent	
CC	cells are also treated for MDR with purine synthesis inhibitors. MTase	
CC	competent and deficient cells are also treated for malignancy with other	
CC	anti-cancer drugs. MTase sequence-specific oligonucleotides can be used	
CC	to detect the presence or absence of MTase in malignant cell lines	
XX		
SQ	Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;	
	Query Match	100.0%; Score 39; DB 2; Length 3083;
	Best Local Similarity	100.0%; Pred. No. 4.7e-05;
	Matches	39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AATATGGCCAGTTTCTGTTTATTACCAAGACATTAA 39	
Db	2838 AATATGGCCAGTTTCTGTTTATTACCAAGACATTAA 2876	
RESULT 13		
ABX10818		
ID	ABX10818 standard; DNA; 3083 BP.	
XX		
AC	ABX10818;	
XX		
DT	17-APR-2003 (first entry)	
XX		
DE	DNA encoding rat methylthioadenosine phosphorylase (MTase).	
XX		
KW	Rat; methylthioadenosine phosphorylase; MTase; detection;	
KW	Rangione method; gene; ds.	
XX		
OS	Rattus sp.	
XX		
FH	Key	Location/Qualifiers
FT	exon	119..151
FT		/*tag= a
FT	intron	/number= 1
FT		152..449
FT		/*tag= b
FT	exon	/number= 1
FT		450..536
FT		/*tag= a
FT	intron	/number= 2
FT		537..723
FT		/*tag= b
FT	exon	/number= 2
FT		724..782
FT		/*tag= a
FT	intron	/number= 3
FT		783..898
FT		/*tag= b
FT	exon	/number= 3
FT		899..1066
FT		/*tag= a
FT	intron	/number= 4
FT		1067..1377

FT /*tag= b
FT /number= 4
FT exon 1378. .1480
FT /*tag= a
FT /number= 5
FT intron 1481. .1763
FT /*tag= b
FT /number= 5
FT exon 1764. .1953
FT /*tag= a
FT /number= 6
FT intron 1954. .2425
FT /*tag= b
FT /number= 6
FT exon 2426. .2548
FT /*tag= a
FT /number= 7
FT intron 2549. .2837
FT /*tag= b
FT /number= 7
FT exon 2838. .2876
FT /*tag= a
FT /number= 8
XX US2002146695-A1.
XX 10-OCT-2002.
XX 09-FEB-2001; 2001US-00780114.
XX 29-DEC-1993; 93US-00176855.
XX 02-JUN-1995; 95US-00459343.
XX 04-MAY-1998; 98US-00072914.
XX
XX (NOBO/) NOBORI T.
XX (CARs/) CARSON D A.
XX (TAKA/) TAKABAYASHI K.
XX Nobori T, Carson DA, Takabayashi K;
XX WPI; 2003-208976/20.
XX
XX Detection of methylthioadenosine phosphorylase presence in mammalian
XX cells, by adding to sample oligonucleotide probes capable of hybridizing
XX to methylthioadenosine phosphorylase encoding nucleic acid.
XX
XX Claim 7; Fig 1; 16pp; English.
XX
XX The invention describes a method of detecting methylthioadenosine
XX phosphorylase (MTase) comprising adding oligonucleotide probes
XX hybridisable to MTase encoding nucleic acid to an assayable sample of
XX cells, where the presence of the nucleic acid indicates the presence of
XX the MTase in a cell. The inventive method is simple and efficient in
XX detecting the presence of MTase in the mammalian cell. The availability
XX of the recombinant MTase enables the production of highly pure material
XX with greater ease and in greater quantities than was obtained using
XX Rangione method for the isolation and purification of native MTase. This
XX sequence encodes rat methylthioadenosine phosphorylase (MTase)
XX
SQ Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;
XX
Query Match 100.0%; Score 39; DB 8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGGCCAGTTTCTGTTTATTACCAAGACATTAA 39
ID AATATGGCCAGTTTCTGTTTATTACCAAGACATTAA 2876

RESULT 14
AAZ35375/C
ID AAZ35375 standard; DNA; 32 BP.

XX
AC AAZ35375;
XX
XX 27-MAR-2000 (first entry)
XX
XX Methylthioadenosine phosphorylase gene exons 5-8 antisense primer.
XX
XX Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis;
XX methylthioadenosine phosphorylase; MTAP; glioma; melanoma;
XX primary lymphoid malignancy; non-small cell lung cancer;
XX head and neck cancer; ovarian cancer; bladder cancer; chondrosarcoma;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO9967634-A1.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US013981.
XX
XX 23-JUN-1998; 98US-0090411P.
XX 17-JUN-1999; 99US-00335231.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Carson DA, Schmid M, Carrera CJ;
XX WPI; 2000-126650/11.
XX
XX
XX Diagnosing and determining prognosis for cancer causitively associated
XX with derangements of chromosome 9p21.
XX
XX
XX Claim 7; Page 16; 55pp; English.
XX
XX This antisense primer is designed for the PCR amplification of exons 5-8
XX of the human methylthioadenosine phosphorylase (MTAP) gene on chromosome
XX 9p21 (see AAZ35351). The primer is used, with a sense primer (see
XX AAZ35374), in a PCR amplification (505 bp product) in step (a) of claimed
XX methods for diagnosis of, and determining a prognosis for, cancer
XX causatively associated with derangements of chromosome 9p21. Step (a) of
XX these methods involves determining whether any portion of the 9p21
XX chromosome including and telomeric to STS 3.21 is deleted, or whether any
XX portion of the gene encoding MTAP is deleted. Step (b) involves
XX determining whether any portion of 9p21 centromeric to STS 3.21 is
XX deleted, or whether any portion of the gene coding for p16 is deleted.
XX The results are indicative of a cancer at an early stage or advanced
XX stage of tumour development. Primer pairs (see AAZ35354-75) are provided
XX for use in the claimed methods, where the cancer is a glioma, primary
XX lymphoid malignancy, non-small cell lung cancer, melanoma, head and neck
XX cancer, ovarian cancer, bladder cancer or a chondrosarcoma (claimed)
XX
SQ Sequence 32 BP; 13 A; 3 C; 7 G; 9 T; 0 U; 0 Other;
XX
Query Match 82.1%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCCAGTTTCTGTTTATTATACCAAGACATTAA 39
ID CCCAGTTTCTGTTTATTATACCAAGACATTAA 1

RESULT 15
ABN87814/C
ID ABN87814 standard; cDNA; 554 BP.

AC ABN87814;

DT 12-AUG-2002 (first entry)

DE Human ovary specific nucleic acid SEQ ID NO:25.

XX

KM Human, ovary specific nucleic acid; OSNA; ovary specific protein; OSP;
KM ovary specific gene; OSG; ovarian cancer; immune response; metastasis;
KM gene; ss.

Homo sapiens.

PN WO200240535-A2.

PD 23-MAY-2002.

PF 20-NOV-2001; 2001WO-US045011.

PR 20-NOV-2000; 2000US-0252061P.

PR 27-NOV-2000; 2000US-0253257P.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Macina RA, Recipon H, Caferkey R, Sun Y, Liu C;

DR WPI; 2002-471617/50.

PT New Ovary specific genes and proteins, useful as a vaccine for treating
PT patients with ovarian cancer, or for diagnosing and monitoring the
PT presence and metastases of ovarian cancer in a patient.

PS Claim 1; Page 169; 260pp; English.

CC ABN87790 to ABN87882 represent human ovary specific nucleic acid (OSNA)
CC sequences, and ABB79297 to ABB79370 represent ovary specific protein
CC (OSP) sequences from the present invention. OSNA and OSP sequences have
CC cytostatic activity, and can be used in vaccine production and gene
CC therapy. An antibody that specifically binds to an OSP can be used for
CC treating a patient with ovarian cancer, particularly for inducing an
CC immune response against the ovarian cancer cell expressing the OSNA or
CC OSP. The OSNAs and OSPs can also be used for diagnosing and monitoring
CC the presence and metastases of ovarian cancer in a patient

SQ Sequence 554 BP; 182 A; 120 C; 136 G; 116 T; 0 U; 0 Other;

Query Match	Score	DB	Length
	59.0%	23	6; 554;

Matches	26;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy	3	TATGCCCCAGTTTCTGTGTTTATTACCAAGA	33
Db	201	TTTGTCACAGTTTCCGTTTCAATACCAAGA	171

Search completed: February 1, 2005, 12:39:37
Job time : 52.1826 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 11.3915 Seconds
(without alignments)
2433.465 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
Sequence: 1 AATATGCCCGAGTTTCTGTTTATTAACAAGACATTAA 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	499	4	US-09-621-976-17307
2	39	100.0	2763	1	US-08-176-413-1
3	39	100.0	2763	2	US-08-612-542B-1
4	39	100.0	2763	2	US-08-772-113-1
5	39	100.0	2763	3	US-09-199-137-1
6	39	100.0	2763	4	US-08-227-800A-14
7	39	100.0	2763	4	US-08-921-954-14
8	39	100.0	2763	5	PCT-US94-14919-1
9	39	100.0	2763	5	PCT-US94-14920-1
10	39	100.0	3083	3	US-08-956-657-1
11	39	100.0	3083	4	US-09-335-231-25
12	32	82.1	32	4	US-09-335-231-24
13	22.6	57.9	168575	4	US-09-426-290-1
14	22	56.4	22	4	US-09-335-231-3
15	21.4	54.9	1120	1	US-08-592-214A-21
16	21.4	54.9	1120	3	US-09-149-976-21
17	21.4	54.9	2421	3	US-08-851-843A-51
18	21.4	54.9	2421	3	US-08-974-549A-218
19	21.4	54.9	2421	3	US-08-854-050-51
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21	21.4	54.9	2421	4	US-09-402-181B-218
22	21.4	54.9	2421	4	US-09-721-456-218
23	21	53.8	6617	4	US-09-976-594-268
24	20.8	53.3	605	4	US-09-270-767-29748
25	20.8	53.3	1023	4	US-09-270-767-13726
26	20.6	52.8	1830121	4	US-09-557-884-1
27	20.6	52.8	1830121	4	US-09-643-990A-1

28	20.6	52.8	1830121	4	US-10-329-960-1	Sequence 1, Appl
29	20.4	52.3	210	4	US-09-489-039A-6656	Sequence 6656, Ap
30	20.4	52.3	900	1	US-08-053-131-182	Sequence 182, App
31	20.4	52.3	900	1	US-08-096-762-182	Sequence 182, App
32	20.4	52.3	900	3	US-09-042-353-45	Sequence 45, Appl
33	20.4	52.3	900	3	US-08-758-417A-310	Sequence 310, Appl
34	20	51.3	799	3	US-09-095-485-1	Sequence 1, Appl
35	20	51.3	1106	5	PCT-US92-02977-5	Sequence 5, Appl
36	20	51.3	1106	5	PCT-US95-03032-4	Sequence 4, Appl
37	20	51.3	1142	4	US-09-556-877-113	Sequence 113, App
38	20	51.3	1142	4	US-09-620-412C-113	Sequence 113, App
39	20	51.3	1142	4	US-09-598-419-113	Sequence 113, App
40	20	51.3	1566	3	US-08-482-073-7	Sequence 7, Appl
41	20	51.3	1698	4	US-09-861-451A-31	Sequence 31, Appl
42	20	51.3	2085	4	US-09-556-877-81	Sequence 81, Appl
43	20	51.3	2085	4	US-09-620-412C-81	Sequence 81, Appl
44	20	51.3	2085	4	US-09-410-568-81	Sequence 81, Appl
45	20	51.3	2085	4	US-09-598-419-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17307
; LENGTH: 499.
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-17307

Query Match 100.0%; Score 39; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTTTATTAACAAGACATTAA 39
Db 359 AATATGCCCGAGTTTCTGTTTATTAACAAGACATTAA 397

RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: No. 5571510ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,413
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD2864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
US-08-176-413-1
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Query Match      100.0%; Score 39; DB 1; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      2272 AATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAA 2310
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RESULT 3
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
; GENERAL INFORMATION:
; APPLICANT: Carrera, Carlos J.
; APPLICANT: Cottam, Howard B.
; APPLICANT: No. 5840505ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
; TITLE OF INVENTION: ACTIVITY IN MALIGNANT METHYLTTHIOADENOSINE PHOSPHORYLASE DEFICI
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,542B
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
```

```
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-08-612-542B-1
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Query Match      100.0%; Score 39; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 AATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAA 39
Db      2272 AATATGCCCCAGTTTCTGTGTTTATTACCAAGACATTAA 2310
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```
RESULT 4
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
; GENERAL INFORMATION:
; APPLICANT: No. 5942393ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,113
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,855
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD3057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
US-08-772-113-1

Query Match      100.0%; Score 39; DB 2; Length 2763;
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Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 2272 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 5

US-09-199-137-1
; Sequence 1, Application US/09199137
; Patent No. 6214571
; GENERAL INFORMATION:
; APPLICANT: No. 6214571ori, Tsutomu
; APPLICANT: Carson, Dennis A.
; APPLICANT: Carrera, Carlos J.
; APPLICANT: Cottam, Howard B.
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,137
; FILING DATE: 24-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD3057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-09-199-137-1
Query Match 100.0%; Score 39; DB 3; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 2272 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 6

US-08-227-800A-14
; Sequence 14, Application US/08227800A

; Patent No. 6689561

; GENERAL INFORMATION:

; APPLICANT: CARSON, DENNIS A.

; APPLICANT: NOBORI, TSUTOMU

; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR

; TITLE OF INVENTION: DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANC

; TITLE OF INVENTION: TREATMENT

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/227,800A

; FILING DATE: 14-APR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: HOWELLS, STACY L.

; REGISTRATION NUMBER: 34,842

; REFERENCE/DOCKET NUMBER: 07340/023001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2763 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; IMMEDIATE SOURCE:

; CLONE: methylthioadenosine Phosphorylase (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..2763

; US-08-227-800A-14

Query Match 100.0%; Score 39; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 2272 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 2310

RESULT 7

US-08-921-954-14

; Sequence 14, Application US/08921954

; Patent No. 6689864

; GENERAL INFORMATION:

; APPLICANT: Carson, Dennis A.

; ADDRESSEE: No. 6689864ori, Tsutomu

; TITLE OF INVENTION: Tumor Suppressor Gene and Methods for

; TITLE OF INVENTION: Detection of Cancer, Monitoring of Tumor Progression and

; TITLE OF INVENTION: Cancer Treatment

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/921,954
;   FILING DATE: 26-Aug-1997
;   CLASSIFICATION: <Unknown>
;
; PRIORITY APPLICATION DATA:
;   APPLICATION NUMBER: US/09/908,671A
;   FILING DATE: 18-Jul-2001
;   APPLICATION NUMBER: US 08/921,954
;   FILING DATE: 20-AUG-1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hirsch, Matthew E.
;   REGISTRATION NUMBER: 47,651
;   REFERENCE/DOCKET NUMBER: 023070-104042US
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2763 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 1..2763
;   OTHER INFORMATION: /note="full-length
;     methylthioadenosine phosphorylase
;     (MTase) genomic nucleotide sequence"
;
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 254..421
;
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 616..720
;
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 964..1203
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

Query Match          100.0%; Score 39; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AATATGCCAGTTTCTGTTTATTATCAAGACATTAA 39
Db      2272 AATATGCCAGTTTCTGTTTATTATCAAGACATTAA 2310

RESULT 8
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
; GENERAL INFORMATION:
;   APPLICANT: THE REGENTS OF THE UNIVERSITY
;   APPLICANT: OF CALIFORNIA
;   TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
;   TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Robbins, Berliner & Carson
;     STREET: 201 N. Figueroa Street, 5th Floor
;     CITY: Los Angeles
;     STATE: California
;     COUNTRY: USA
;     ZIP: 90012
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
```

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/14919
;   FILING DATE:
;   CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Berliner, Robert
;   REGISTRATION NUMBER: 20,121
;   REFERENCE/DOCKET NUMBER: 5555-286
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 213-977-1001
;   TELEFAX: 213-977-1003
;
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2763 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   IMMEDIATE SOURCE:
;   CLONE: methyladenosine phosphatase
;
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..2763
;
; PCT-US94-14919-1

Query Match          100.0%; Score 39; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AATATGCCAGTTTCTGTTTATTATCAAGACATTAA 39
Db      2272 AATATGCCAGTTTCTGTTTATTATCAAGACATTAA 2310

RESULT 9
PCT-US94-14920-1
; Sequence 1, Application PC/TUS9414920
; GENERAL INFORMATION:
;   APPLICANT: THE REGENTS OF THE UNIVERSITY
;   APPLICANT: OF CALIFORNIA
;   TITLE OF INVENTION: METHOD FOR DETECTION OF
;   TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Robbins, Berliner & Carson
;     STREET: 201 N. Figueroa Street, 5th Floor
;     CITY: Los Angeles
;     STATE: California
;     COUNTRY: USA
;     ZIP: 90012
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US94/14920
;     FILING DATE:
;     CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;     NAME: Berliner, Robert
;     REGISTRATION NUMBER: 20,121
;     REFERENCE/DOCKET NUMBER: 5555-287
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 213-977-1001
;       TELEFAX: 213-977-1003
;
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2763 base pairs
;     TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14920-1

Query Match 100.0%; Score 39; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 39
Db 2272 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 2310

RESULT 10

US-08-956-657-1
; Sequence 1, Application US/08956657
; Patent No. 6210917
; GENERAL INFORMATION:
; APPLICANT: NO. 6210917ori et al., Tautomu
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,342
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/050001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3083 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-956-657-1

Query Match 100.0%; Score 39; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 39
Db 2838 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 2876

RESULT 11

US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTAP) gene
; NAME/KEY: modified base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
; US-09-335-231-25

Query Match 100.0%; Score 39; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 39
Db 2838 AATATGCCAGTTTCTGTTTATTAACCAAGACATTAA 2876

RESULT 12

US-09-335-231-24/c
; Sequence 24, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.

```
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-sense
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US-09-335-231-24
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Query Match      82.1%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 CCCAGTTTCTGTTTATTATACCAAGACATTAA 39
Db      32 CCCAGTTTCTGTTTATTATACCAAGACATTAA 1
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```
RESULT 13
US-09-426-290-1/c
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 168575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21181)...(21403)
; NAME/KEY: CDS
; LOCATION: (95252)...(95430)
; NAME/KEY: CDS
; LOCATION: (101753)...(101996)
; NAME/KEY: CDS
; LOCATION: (110324)...(110439)
; NAME/KEY: CDS
; LOCATION: (124058)...(124278)
; NAME/KEY: CDS
; LOCATION: (127009)...(127130)
; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
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US-09-426-290-1
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Query Match      57.9%; Score 22.6; DB 4; Length 168575;
Best Local Similarity 75.7%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY      2 ATATGCCCAAGTTTCTGTTTATTATACCAAGACATTAA 38
Db      60300 ATATGGTACATTTTCTCTTCTTTCCAGAAAGTA 60264
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RESULT 14
US-09-335-231-3
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; Sequence 3, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sense primer
;
US-09-335-231-3
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Query Match      56.4%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      11 AGTTTCTGTTTATTATACCAAG 32
Db      1 AGTTTCTGTTTATTATACCAAG 22
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RESULT 15
US-08-592-214A-21
; Sequence 21, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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NAME/KEY: unsure
LOCATION: 389..393
OTHER INFORMATION: /note= "N" = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: unsure
LOCATION: 810..814
OTHER INFORMATION: /note= "N" = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: unsure
LOCATION: 1118..1120
OTHER INFORMATION: /note= "N" = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1120
OTHER INFORMATION: /note= "sequence = Brassica
OTHER INFORMATION: oleracea CAL gene"
US-08-592-214A-21

Query Match 54.9%; Score 21.4; DB 1; Length 1120;
Best Local Similarity 71.8%; Pred. No. 31;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 AATATGCCCCAGTTTCTGTTTATTACCAAGACATTAA 39
Db 769 AAGATTGAATAGTCTGTGTTTATTACATAACATGAA 807

Search completed: February 1, 2005, 15:01:04
Job time : 14.3915 secs

This Page Blank (uspto)

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 53.6349 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876

Perfect score: 39
Sequence: 1 AATATGCCAGTTTCTGTTTATTATCCAGACATTAA 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	39	100.0	603	11	US-09-969-034-3235 Sequence 3235, Ap
C 2	39	100.0	870	16	US-10-367-366-1 Sequence 1, Appli
C 3	39	100.0	1437	15	US-10-106-698-749 Sequence 749, App
C 4	39	100.0	2269	18	US-10-779-476-2 Sequence 2, Appli
C 5	39	100.0	2763	10	US-09-908-671-14 Sequence 14, Appl
C 6	39	100.0	3083	9	US-09-780-114-1 Sequence 1, Appli
C 7	39	100.0	3083	15	US-10-326-681-25 Sequence 25, Appl
C 8	32	82.1	32	15	US-10-326-681-24 Sequence 24, Appl
C 9	24	61.5	678	13	US-10-027-632-29328 Sequence 29328, A
C 10	24	61.5	678	13	US-10-027-632-29329 Sequence 29329, A
C 11	24	61.5	678	15	US-10-027-632-29328 Sequence 29328, A
C 12	24	61.5	678	15	US-10-027-632-29329 Sequence 29329, A

C 13	24	61.5	808	13	US-10-027-632-31882	Sequence 31882, A
C 14	24	61.5	808	15	US-10-027-632-31882	Sequence 31882, A
C 15	23	59.0	554	15	US-10-076-747-54	Sequence 54, Appl
C 16	23	59.0	554	16	US-10-001-885-25	Sequence 25, Appl
C 17	22.6	57.9	1213	13	US-10-027-632-123022	Sequence 123022,
C 18	22.6	57.9	1213	13	US-10-027-632-123023	Sequence 123023,
C 19	22.6	57.9	1213	15	US-10-027-632-123022	Sequence 123022,
C 20	22.6	57.9	1213	15	US-10-027-632-123023	Sequence 123023,
C 21	22.6	57.9	168575	15	US-10-178-194-1	Sequence 1, Appli
C 22	22	56.4	22	15	US-10-326-681-3	Sequence 3, Appli
C 23	22	56.4	643	13	US-10-027-632-150817	Sequence 150817,
C 24	22	56.4	643	15	US-10-027-632-150817	Sequence 150817,
C 25	21.8	55.9	622	13	US-10-027-632-219425	Sequence 219425,
C 26	21.8	55.9	622	15	US-10-027-632-219425	Sequence 219425,
C 27	21.8	55.9	1603	13	US-10-027-632-97331	Sequence 97331, A
C 28	21.8	55.9	1603	13	US-10-027-632-97332	Sequence 97332, A
C 29	21.8	55.9	1603	15	US-10-027-632-97331	Sequence 97331, A
C 30	21.8	55.9	1603	15	US-10-027-632-97332	Sequence 97332, A
C 31	21.6	55.4	429	16	US-10-424-599-48727	Sequence 48727, A
C 32	21.6	55.4	2890	13	US-10-027-632-256650	Sequence 256650,
C 33	21.6	55.4	2890	13	US-10-027-632-256651	Sequence 256651,
C 34	21.6	55.4	2890	15	US-10-027-632-256650	Sequence 256650,
C 35	21.6	55.4	2890	15	US-10-027-632-256651	Sequence 256651,
C 36	21.6	55.4	49088	13	US-10-087-192-13	Sequence 13, Appl
C 37	21.6	55.4	56773	18	US-10-331-053-47	Sequence 47, Appl
C 38	21.6	55.4	194049	13	US-10-087-192-1495	Sequence 1495, Ap
C 39	21.6	55.4	302250	9	US-09-962-832-154	Sequence 154, Appl
C 40	21.4	54.9	577	15	US-10-409-643-10	Sequence 244523,
C 41	21.4	54.9	689	13	US-10-027-632-244523	Sequence 244523,
C 42	21.4	54.9	689	15	US-10-027-632-244523	Sequence 244523,
C 43	21.4	54.9	1062	9	US-09-938-842A-1639	Sequence 1639, Ap
C 44	21.4	54.9	1062	11	US-09-938-842A-1639	Sequence 1639, Ap
C 45	21.4	54.9	1240	16	US-10-425-114-7600	Sequence 7600, Ap

ALIGNMENTS

RESULT 1
US-09-969-034-3235/C
; Sequence 3235, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthachi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969, 034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237, 271
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3235
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 492, 497, 506, 527, 542, 544, 573, 576, 597
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3235
Query Match 100.0%; Score 39; DB 11; Length 603;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39
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Db 432 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 394

RESULT 2

US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Pei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skaltzky, Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; FILE REFERENCE: PC19080A (AG110-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1

Query Match 100.0%; Score 39; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39
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Db 820 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 858

RESULT 3

US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-749

Query Match 100.0%; Score 39; DB 15; Length 1437;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39

Db 120 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 158
|||||

RESULT 4

US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
; APPLICANT: Salmedix, Inc.
; APPLICANT: Leoní, Lorenzo M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
; FILE REFERENCE: 076936-0307942
; CURRENT APPLICATION NUMBER: US/10/779,476
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,888
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/460,715
; PRIOR FILING DATE: 2004-04-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-476-2

Query Match 100.0%; Score 39; DB 18; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 39
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Db 935 AATATGCCCCAGTTTCTGTTTATTATACCAAGACATTAA 973

RESULT 5

US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; NOBORI, TSUTOMU
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
; DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
; TREATMENT
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,671
; FILING DATE: 18-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,800
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/023001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: Methylthiadenosine Phosphorylase (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

Query Match 100.0%; Score 39; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTATTATACCAAGACATTAA 39
Db 2272 AATATGCCCGAGTTTCTGTATTATACCAAGACATTAA 2310

RESULT 6
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020146695A1or1, Tsutomu
; Carson, Dennis A.
; Takabayashi, Kenji
; TITLE OF INVENTION: Method for Detection of the Presence or
; Absence of Methylthiadenosine Phosphorylase
; (MTase) in a
; Cell Sample by Detection of the Presence or Absence
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,114
; FILING DATE: 09-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,914
; FILING DATE: 04-May-1998
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: US 08/459,343
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 08/827,342
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baetian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-103030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3083 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..3083
OTHER INFORMATION: /note= "rat methylthiadenosine
phosphorylase (MTase)"
FEATURE:
NAME/KEY: exon
LOCATION: 119..151
OTHER INFORMATION: /note= "exon 1"
FEATURE:
NAME/KEY: exon
LOCATION: 450..536
OTHER INFORMATION: /note= "exon 2"
FEATURE:
NAME/KEY: exon
LOCATION: 724..782
OTHER INFORMATION: /note= "exon 3"
FEATURE:
NAME/KEY: exon
LOCATION: 899..1066
OTHER INFORMATION: /note= "exon 4"
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1480
OTHER INFORMATION: /note= "exon 5"
FEATURE:
NAME/KEY: exon
LOCATION: 1764..1953
OTHER INFORMATION: /note= "exon 6"
FEATURE:
NAME/KEY: exon
LOCATION: 2426..2548
OTHER INFORMATION: /note= "exon 7"
FEATURE:
NAME/KEY: exon
LOCATION: 2838..2876
OTHER INFORMATION: /note= "exon 8"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

Query Match 100.0%; Score 39; DB 9; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCGAGTTTCTGTATTATACCAAGACATTAA 39
Db 2838 AATATGCCCGAGTTTCTGTATTATACCAAGACATTAA 2876

RESULT 7
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/10/326,681
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/090,411
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083

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/
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: genomic sequence for methylthioadenosine
/ OTHER INFORMATION: phosphorylase (MTAP) gene
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (1)..(3083)
/ OTHER INFORMATION: n = unknown
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (119)..(151)
/ OTHER INFORMATION: exon 1
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (450)..(536)
/ OTHER INFORMATION: exon 2
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (724)..(782)
/ OTHER INFORMATION: exon 3
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (899)..(1066)
/ OTHER INFORMATION: exon 4
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (1378)..(1480)
/ OTHER INFORMATION: exon 5
/ FEATURE:
/ NAME/KEY: (1764)..(1953)
/ LOCATION: (1764)..(1953)
/ OTHER INFORMATION: exon 6
/ FEATURE:
/ NAME/KEY: (2426)..(2548)
/ LOCATION: (2426)..(2548)
/ OTHER INFORMATION: exon 7
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (2838)..(2876)
/ OTHER INFORMATION: exon 8
/ US-10-326-681-25

Query Match          100.0%; Score 39; DB 15; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      2838 AATATGCCAGTTTCTGTTTATTAACAAGACATTAA 2876
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RESULT 8
US-10-326-681-24/c
; Sequence 24, Application US/10326681
; Publication No. US20030175768A1
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/10/326,681
; FILE FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 32
; TYPE: DNA
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/
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:anti-sense
/ OTHER INFORMATION: primer
/ US-10-326-681-24
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Query Match          82.1%; Score 32; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      8 CCCAGTTTCTGTTTATTAACAAGACATTAA 39
Db      32 CCCAGTTTCTGTTTATTAACAAGACATTAA 1
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RESULT 9
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29328
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-29328
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Query Match          61.5%; Score 24; DB 13; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy      3 TATGCCAGTTTCTGTTTATTAACAAGAC 34
Db      324 TATGCCAGTTTCTGTTTACTGAGAAAGC 293
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RESULT 10
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329
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Query Match      61.5%; Score 24; DB 13; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 TATGCCCAGTTTCTGTTTATTACCAAGAC 34
Db      324 TATGCCCAGTTTCTGTTTACTGAGAAGC 293
```

RESULT 11

```
US-10-027-632-29328/c
; Sequence 29328, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29328
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29328
```

```
Query Match      61.5%; Score 24; DB 15; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 TATGCCCAGTTTCTGTTTATTACCAAGAC 34
Db      324 TATGCCCAGTTTCTGTTTACTGAGAAGC 293
```

```
RESULT 12
US-10-027-632-29329/c
; Sequence 29329, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29329
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-29329
```

```
Query Match      61.5%; Score 24; DB 15; Length 678;
Best Local Similarity 84.4%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      3 TATGCCCAGTTTCTGTTTATTACCAAGAC 34
Db      324 TATGCCCAGTTTCTGTTTACTGAGAAGC 293
```

RESULT 13

```
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31882
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-31882
```

```
Query Match      61.5%; Score 24; DB 13; Length 808;
Best Local Similarity 84.4%; Pred. No. 40;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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OY 3 TATGCCCCAGTTTCTGTGTTTATTACCAAGAC 34
| | | | | | | | | | | | | | | | | | | | | |
Db 324 TATGCCCCAGTTTCTGTGTTTACTGAGAGGC 293

RESULT 14
US-10-027-632-31882/c
; Sequence 31882, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 31882
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-31882

Query Match 61.5%; Score 24; DB 15; Length 808;
Best Local Similarity 84.4%; Pred. No. 40;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TATGCCCCAGTTTCTGTGTTTATTACCAAGAC 34
| | | | | | | | | | | | | | | | | | | | | |
Db 324 TATGCCCCAGTTTCTGTGTTTACTGAGAGGC 293

RESULT 15
US-10-076-747-54/c
; Sequence 54, Application US/10076747
; Publication No. US20030180726A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Kaira, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and F
; FILE REFERENCE: DEX-0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; PRIOR APPLICATION NUMBER: 2002-02-13
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/268,834
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 554

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-076-747-54

Query Match 59.0%; Score 23; DB 15; Length 554;
Best Local Similarity 83.9%; Pred. No. 87;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 TATGCCCCAGTTTCTGTGTTTATTACCAAGA 33
| | | | | | | | | | | | | | | | | | | | | |
Db 201 TTGTCGCCAGTTTCCGTTCAATACCAAGA 171

Search completed: February 1, 2005, 17:20:32
Job time : 54.6349 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 438.493 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2838_2876
Perfect score: 39
Sequence: 1 AATATGCCAGCTTCTGTTTATTACCAAGACATTAA 39

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	257	1 AI919501	AI919501 tp22b01.x
2	39	100.0	358	2 BE768971	BE768971 PM4-FT002
3	39	100.0	401	1 AI674711	AI674711 wd19e10.x
4	39	100.0	491	1 AA635142	AA635142 af10e10.s
5	39	100.0	568	7 C0586973	C0586973 DG2-13911
6	39	100.0	570	6 CD364939	CD364939 UI-H-FT2-
7	39	100.0	600	7 C0701132	C0701132 DG32-195b
8	39	100.0	612	7 CN409515	CN409515 170006001
9	39	100.0	638	7 CN409513	CN409513 170005327
10	39	100.0	681	4 BM784030	BM784030 K-EST0062
11	39	100.0	684	6 CD364946	CD364946 UI-H-FT2-
12	39	100.0	819	2 BF981023	BF981023 602310222
13	39	100.0	836	1 AL048242	AL048242 DKFZp5860
14	39	100.0	836	4 BG574734	BG574734 602596770
15	39	100.0	900	5 BX390237	BX390237 BX390237
16	39	100.0	903	5 BX350035	BX350035 BX350035
17	39	100.0	911	5 BX371508	BX371508 BX371508
18	39	100.0	950	7 CF413058	CF413058 CH3#083 G
19	39	100.0	975	4 BM472910	BM472910 AGENCOURT
20	39	100.0	1064	5 BX459089	BX459089 BX459089
21	39	100.0	1380	3 BC012316	BC012316 Homo sapi
22	38.6	99.0	1075	1 AL543068	AL543068 AL543068
23	37	94.9	659	4 BG572739	BG572739 602594259
24	36	92.3	330	5 BX102948	BX102948 BX102948

25	35.8	91.8	388	1 AJ686857	AJ686857
26	35.8	91.8	421	1 AJ667166	AJ667166
27	35.8	91.8	429	1 AV667881	AV667881
28	35.8	91.8	477	4 BG938257	BG938257
29	35.8	91.8	484	7 CF930825	CF930825
30	35.8	91.8	562	4 BI774611	BI774611
31	35.8	91.8	581	6 CB538214	CB538214
32	35.8	91.8	586	7 CN441464	CN441464
33	35.8	91.8	648	5 BQ599498	BQ599498
34	35.8	91.8	682	7 CN788377	CN788377
35	34	87.2	127	1 AA503765	AA503765
36	33.2	85.1	609	6 CD535426	CD535426
37	33	84.6	205	2 BF431095	BF431095
38	32.6	83.6	303	6 CA535795	CA535795
39	32.6	83.6	351	6 CF269885	CF269885
40	32.6	83.6	429	4 BG797326	BG797326
41	32.6	83.6	443	6 CA536077	CA536077
42	32.6	83.6	529	6 CB545374	CB545374
43	32.6	83.6	541	6 CA533816	CA533816
44	32.6	83.6	546	7 CK333529	CK333529
45	32.6	83.6	557	7 CK364324	CK364324

ALIGNMENTS

RESULT 1
AI919501/c 257 bp mRNA linear EST 14-DEC-1999
LOCUS tp22b01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188489 3'
DEFINITION similar to SW:MTAP HUMAN Q13126 5'-METHYLTHIOADENOSINE
PHOSPHORYLASE ;, mRNA sequence.

ACCESSION AI919501
VERSION AI919501.1 GI:5639356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 257)

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/JNL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 246.
location/Qualifiers

1. 257
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2188489"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN

Query Match 100.0%; Score 39; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 39
|||||
Db 119 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 81

RESULT 2
BE768971 358 bp mRNA linear EST 20-SEP-2000
LOCUS PM4-FT0023-020600-001-d09 FT0023 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE768971
ACCESSION BE768971
VERSION BE768971.1 GI:10222629
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=ct2=PM4-FT0023-020600-001-d09&ct3=2000-06-02&cl=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 358.

FEATURES

source 1. 358
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FT0023"
/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 39; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 39
|||||
Db 48 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 86

RESULT 3

AI674711/c 401 bp mRNA linear EST 19-MAY-1999
LOCUS AI674711
DEFINITION wd19e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328618 3' similar to SW:MTAP HUMAN Q13126 5'-METHYLTHIOADENOSINE PHOSPHORYLASE ;, mRNA sequence.

ACCESSION AI674711
VERSION AI674711.1 GI:4875191
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.

FEATURES
source 1. 401
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2328618"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bernaldo."

ORIGIN

Query Match 100.0%; Score 39; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 39
|||||
Db 247 AATATGCCAGTTTCTGTTTATTACCAACATTTAA 209

RESULT 4
AA635142/c 491 bp mRNA linear EST 21-OCT-1997
LOCUS AA635142
DEFINITION af10e10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031274 3' similar to TR:G847724 G847724 METHYLTHIOADENOSINE PHOSPHORYLASE ;, mRNA sequence.
ACCESSION AA635142
VERSION AA635142.1 GI:2558356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washu-NCI human EST Project
JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 289.
Location/Qualifiers

FEATURES
source
1..491
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1031274"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCCGCAATTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Benito Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 39; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCCCGAGTTTCTGTTTATTATACCAAGACATTAA 39
|||||
Db 371 AATATGCCCGAGTTTCTGTTTATTATACCAAGACATTAA 333

RESULT 5
COS86973/c 568 bp mRNA linear EST 21-JUL-2004
LOCUS DG2-139111 DG2-brain Canis familiaris cDNA 3', mRNA sequence.
DEFINITION COS86973
ACCESSION COS86973
VERSION COS86973.1 GI:50432494
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 568)
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuetz, D., Kranz, H.,
Henrich, J., and Loebbert, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schluter
LION Bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.
Location/Qualifiers

FEATURES
source
1..568
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B"

/clone_lib="DG2-brain"
/note="Organ: brain; Vector: Dog pBluescript LION"

ORIGIN

Query Match 100.0%; Score 39; DB 7; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCCCGAGTTTCTGTTTATTATACCAAGACATTAA 39
|||||
Db 379 AATATGCCCGAGTTTCTGTTTATTATACCAAGACATTAA 341

RESULT 6
CD364939/c 570 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FT2-bjn-i-17-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
DEFINITION UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.
ACCESSION CD364939
VERSION CD364939.1 GI:31149029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers

FEATURES
source
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-i-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP_FT2 is a subtrated cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph
aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours;
Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt
adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24
hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
The library was subtrated according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. The tissue
was provided by Dr. Gary W. Hunninghake of the University

of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GCCCATGCCG"

ORIGIN

Query Match 100.0%; Score 39; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
404 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 366

Db

RESULT 7

LOCUS CO701132/c 600 bp mRNA linear EST 26-JUL-2004
DEFINITION DG32-195b11 DG32-liver Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO701132
VERSION CO701132.1 GI:50649800
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS Schluter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
Henrich,J. and Loebbert,R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schluter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schluter@lionbioscience.com.

FEATURES
source location/Qualifiers
1..600
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DHL0B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: Dog pBluescript LION"

ORIGIN

Query Match 100.0%; Score 39; DB 7; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
359 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 321

Db

RESULT 8
LOCUS CN409515 612 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600188932 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409515
VERSION CN409515.1 GI:47396639
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,

TITLE Lebkowski,J and Stanton,L.W.
JOURNAL Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 612 Std Error: 0.00.
location/Qualifiers
1..612
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Query Match 100.0%; Score 39; DB 7; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
230 AATATGCCCCAGTTTCTGTTTATTATCCAGACATTAA 268

Db

RESULT 9
LOCUS CN409513 638 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409513
VERSION CN409513.1 GI:47396637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 638 Std Error: 0.00.
location/Qualifiers
1..638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="Oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

JOURNAL
COMMENT

FEATURES

source

ORIGIN

QY 1 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
Db 404 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 366

RESULT 12
BF981023 819 bp mRNA linear EST 23-JAN-2001
LOCUS 602310222F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4401533 5',
DEFINITION mRNA sequence.
ACCESSION BF981023
VERSION BF981023.1 GI:12383835
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10108 row: k column: 06
High quality sequence stop: 667.
location/Qualifiers
1..819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4401533"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 39; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
Db 115 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 153

RESULT 13
AL048242 836 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp58601023_r1 586 (synonym: hute1) Homo sapiens cDNA clone
DEFINITION DKFZp58601023, mRNA sequence.
ACCESSION AL048242
VERSION AL048242.1 GI:4729075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS Ansoerge,W., Winkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Ansoerge, et al.)
JOURNAL Unpublished (1999)

COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp58601023) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
1..836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp58601023"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="586 (synonym: hute1)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

ORIGIN
Query Match 100.0%; Score 39; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 39
|||||
Db 321 AATATGCCCAGTTTCTGTTTATTATCCAGACATTAA 359

RESULT 14
BG574734 836 bp mRNA linear EST 10-APR-2001
LOCUS BG574734
DEFINITION 602596770F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705673 5',
mRNA sequence.
ACCESSION BG574734
VERSION BG574734.1 GI:13582387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10572 row: k column: 18
High quality sequence stop: 680.
location/Qualifiers
1..836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4705673"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dt primed."

Average insert size 1,383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 39; DB 4; Length 836;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 22 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 60

RESULT 15

BX390237 900 bp mRNA linear EST 28-APR-2004
LOCUS BX390237
DEFINITION BX390237 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI002YH04 5-PRIME, mRNA sequence.

ACCESSION BX390237
VERSION BX390237
KEYWORDS BX390237.2 GI:46834877
EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 900)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30461423.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BAG024ZA09_CS02273_1&c=5445.f

FEATURES

Source location/Qualifiers
1..900
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI002YH04"
/tissue="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 39; DB 5; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 39
|||||
Db 58 AATATGCCAGTTTCTGTTTATTACCAAGACATTAA 96

Search completed: February 1, 2005, 14:58:29
Job time : 439.493 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 691.095 Seconds
(without alignments)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548

Perfect score: 123
Sequence: 1 GTTTCGGTGACCGGCTCTT.....AAACCTCCATTAACCTGAAG 123

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	123	100.0	303	9	AH013410S7	L42633 Homo sapien
2	123	100.0	499	6	AR425810	AR425810 Sequence
3	123	100.0	499	6	AX986504	AX986504 Sequence
4	123	100.0	499	6	BD121363	BD121363 EST and e
5	123	100.0	849	9	CR541710	CR541710 Homo sapi
6	123	100.0	852	9	CR541670	CR541670 Homo sapi
7	123	100.0	870	6	AX826996	AX826996 Sequence
8	123	100.0	1021	9	L40432	L40432 Homo sapien
9	123	100.0	1890	9	BC026106	BC026106 Homo sapi
10	123	100.0	2269	9	HSU22233	U22233 Human methy
11	123	100.0	2763	6	AR059583	AR059583 Sequence
12	123	100.0	2763	6	I28320	I28320 Sequence 1
13	123	100.0	2763	6	AR473576	AR473576 Sequence
14	123	100.0	2763	6	AR474046	AR474046 Sequence
15	123	100.0	3083	6	AR144466	AR144466 Sequence
16	123	100.0	3083	6	AR342446	AR342446 Sequence
17	123	100.0	168656	9	AL359922	AL359922 Human DNA
18	123	100.0	250000	9	AB060808	AB060808 Homo sapi
19	100.6	81.8	807	9	L42635	L42635 Homo sapien

C	20	100.6	81.8	94125	9	AC016966	AC016966 Homo sapi
C	21	100.6	81.8	168366	2	AC069409	AC069409 Homo sapi
C	22	100.6	81.8	180606	2	AC073406	AC073406 Homo sapi
C	23	95.8	77.9	1055	10	AB056100	AB056100 Mus muscu
C	24	95.8	77.9	2565	10	BC003858	BC003858 Mus muscu
C	25	95.8	77.9	194025	10	AL831719	AL831719 Mouse DNA
C	26	94.2	76.6	225782	2	AC109529	AC109529 Rattus no
C	27	94.2	76.6	287775	2	AC108638	AC108638 Rattus no
C	28	88.2	71.7	170899	2	AC144208	AC144208 Macaca mu
C	29	60.4	49.1	230762	2	AC097556	AC097556 Rattus no
C	30	60.4	49.1	232771	2	AC128406	AC128406 Rattus no
C	31	55	44.7	151290	10	AC121902	AC121902 Mus muscu
C	32	52.4	42.6	90801	9	AC025033	AC025033 Homo sapi
C	33	52.4	42.6	146349	2	AC012027	AC012027 Homo sapi
C	34	52.4	42.6	171615	2	AC089988	AC089988 Homo sapi
C	35	52.4	42.6	212382	2	AC010936	AC010936 Homo sapi
C	36	50	40.7	8319	5	FRU250231	AJ250231 Fugu rubr
C	37	46.2	37.6	1255	5	BC056545	BC056545 Dario rer
C	38	46.2	37.6	1265	5	BC046035	BC046035 Dario rer
C	39	46.2	37.6	150073	5	BX323448	BX323448 Zebrafish
C	40	46.2	37.6	161859	2	CR385087	CR385087 Dario rer
C	41	46.2	37.6	245135	2	AC095099	AC095099 Rattus no
C	42	34.2	27.8	236746	2	AC119312	AC119312 Rattus no
C	43	34	27.6	174697	9	AP002370	AP002370 Homo sapi
C	44	34	27.6	184516	2	AC018708	AC018708 Homo sapi
C	45	34	27.6	197847	9	AP002751	AP002751 Homo sapi

ALIGNMENTS

RESULT 1	AH013410S7	303 bp	DNA	linear	PRI 01-DEC-2003
LOCUS	AH013410S7				
DEFINITION	Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 7.				
ACCESSION	L42633				
VERSION	L42633.1	GI:38570313			
KEYWORDS					
SEGMENT	7 of 8				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.				
AUTHORS	1 (bases 1 to 303)				
TITLE	Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)				
MEDLINE	96234115				
PUBMED	8650244				
FEATURES					
source	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/chromosome="9"				
	/map="9p22-p21"				
	/clone="CM15"				
	/tissue type="Placenta"				
	76..198				
	/gene="MTAP"				
	/note="putative"				
	/number=7				

ORIGIN

Query Match	100.0%;	Score 123;	DB 9;	length 303;
Best Local Similarity	100.0%;	Pred. No. 1.7e-28;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	1	GTTTCGGTGACCGGCTCTTAAGACCTGAAGAAACGCTAATAAAGCCAAAGCTTA	60	
	76	GTTTCGGTGACCGGCTCTTAAGACCTGAAGAAACGCTAATAAAGCCAAAGCTTA	135	

QY	61	CTGCTCACTACCATACCTAGATAGGGGTCCACAGAAATGGTCAGAAAACCCCTCCATAACTTG	120
Db	136	CTGCTCACTACCATACCTAGATAGGGGTCCACAGAAATGGTCAGAAAACCCCTCCATAACTTG	195
QY	121	AAG 123	
Db	196	AAG 198	
RESULT 2			
LOCUS	AR425810	499 bp	DNA
DEFINITION	Sequence 17307 from patent US 6639063.		linear
ACCESSION	AR425810		
VERSION	AR425810.1	GI:40180920	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 499)		
TITLE	Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.		
JOURNAL	EST's and encoded human proteins		
FEATURES	Patent: US 6639063-A 17307 28-OCT-2003;		
	Location/Qualifiers		
	1..499		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	100.0%;	Score 123;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 1.6e-28;	Length 499;
Matches	123;	Conservative 0;	Mismatches 0;
		Indels 0;	Gaps 0;
QY	1	GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA	60
Db	236	GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA	295
QY	61	CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGGTCAGAAAACCCCTCCATAACTTG	120
Db	296	CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGGTCAGAAAACCCCTCCATAACTTG	355
QY	121	AAG 123	
Db	356	AAG 358	
RESULT 3			
LOCUS	AX986504	499 bp	DNA
DEFINITION	Sequence 17307 from Patent EP1104808.		linear
ACCESSION	AX986504		
VERSION	AX986504.1	GI:40992644	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.		
TITLE	ESTs and encoded human proteins		
JOURNAL	Patent: EP 1104808-A 17307 06-JUN-2001;		
FEATURES	Genset (FR)		
	Location/Qualifiers		
	1..499		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match	100.0%;	Score 123;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 1.6e-28;	Length 499;
Matches	123;	Conservative 0;	Mismatches 0;
		Indels 0;	Gaps 0;

QY	1	GTTCGGTGACCGGGTCTTTAAAGACCCCTGAAGAAACAAACGCTAATAAAGCCAAAGCTTA	60
Db	236	GTTCGGTGACCGGGTCTTTAAAGACCCCTGAAGAAACAAACGCTAATAAAGCCAAAGCTTA	295
QY	61	CTGCTCACTACCACTAAGGTCAGATAGGGTCCACAGAAATGGTCAGAAAACCTCCATAACCTG	120
Db	296	CTGCTCACTACCACTAAGGTCAGATAGGGTCCACAGAAATGGTCAGAAAACCTCCATAACCTG	355
QY	121	AAG 123	
Db	356	AAG 358	
RESULT 4			
BD121363	BD121363	499 bp	DNA linear PAT 18-SEP-2002
LOCUS	BD121363		
DEFINITION	EST and encoded human protein.		
ACCESSION	BD121363		
VERSION	BD121363.1	GI:23216273	
KEYWORDS	JP 2002010789-A/13440.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 499)		
TITLE	Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.		
JOURNAL	EST and encoded human protein		
	Patent: JP 2002010789-A 13440 15-JAN-2002;		
	GENSET CORP		
COMMENT	OS Homo sapiens (human)		
	PN JP 2002010789-A/13440		
	PD 15-JAN-2002		
	PR 07-AUG-2000 JP 2000280989		
	PR 05-AUG-1999 US 60/147499		
	PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO		
	PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21, PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC C12N15/00		
	CC EST and encoded human protein		
	CC Key location/Qualifiers		
	FT source 1..499		
	FT Location/Qualifiers		
FEATURES	1..499		
source	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
	Query Match	100.0%;	Score 123; DB 6; Length 499;
	Best Local Similarity	100.0%;	Pred. No. 1.6e-28;
	Matches 123; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	GTTCGGTGACCGGGTCTTTAAAGACCCCTGAAGAAACAAACGCTAATAAAGCCAAAGCTTA	60
Db	236	GTTCGGTGACCGGGTCTTTAAAGACCCCTGAAGAAACAAACGCTAATAAAGCCAAAGCTTA	295
QY	61	CTGCTCACTACCACTAAGGTCAGATAGGGTCCACAGAAATGGTCAGAAAACCTCCATAACCTG	120
Db	296	CTGCTCACTACCACTAAGGTCAGATAGGGTCCACAGAAATGGTCAGAAAACCTCCATAACCTG	355
QY	121	AAG 123	
Db	356	AAG 358	
RESULT 5			
LOCUS	CR541710	849 bp	mRNA linear PRI 29-JUN-2004
DEFINITION	Homo sapiens full open reading frame cDNA clone RZPDo834H1128D for		

gene MTAP, methylthioadenosine phosphorylase; complete cds, without stopcodon.

ACCESSION CR541710
VERSION CR541710.1 GI:49456380
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Halleck,A., Ebert,L., Mfoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and Labaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 849)
AUTHORS Halleck,A., Ebert,L., Mfoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and Labaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPD0834H1128D, ORFNO 3404
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834H1128D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showlib.pl.cgi?response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD; Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH131058.01L
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found AA exchange(s) at position (first base of changed triplet): 133(1eu->ser) 166(1le->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.location/Qualifiers

FEATURES
Source 1. 849
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834H1128D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
1. 849
/gene="MTAP"
1. .>849
/gene="MTAP"
/codon_start=1
/protein_id="CAG46511.1"
/db_xref="GI:49456381"
/translation="MASGTTTAVKIGIIGTGLDDPEILEGRTEKYVDTPFGKPSDA
SLGKIKNVDCVLLARHGROHTIPMSKVNYQANIMALKEGCTHIVTTACGSLREI
QPGDIVIIDQFIDRTTMRPQSFYDGSWSCARGVCHIPMAEPFCPKTREVLLETAKLIG
LRCHSKGTMTVIEGPRFSSRAESFMERTWGADVIMNTVPEVTLAKEAGICYSASIMA

TDYDCWKEHEAVSVDRVLTLEKENANKAKSLTLTTPQIGSTWSETLHNLKNAQF SVLLPRH"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 849;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 60
|||||
DB 691 GTTTCGGTGACCGGGTCTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 750
|||||

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCTCCATAACCTG 120
|||||
DB 751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAACCTCCATAACCTG 810
|||||

QY 121 AAG 123
|||
DB 811 AAG 813

RESULT 6
CR541670
LOCUS CR541670
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834G1127D for gene MTAP, methylthioadenosine phosphorylase; complete cds, incl. stopcodon.
ACCESSION CR541670
VERSION CR541670.1 GI:49456300
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Halleck,A., Ebert,L., Mfoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and Labaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 852)
AUTHORS Halleck,A., Ebert,L., Mfoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and Labaer,J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT RZPD; RZPD0834G1127D, ORFNO 3305
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834G1127D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showlib.pl.cgi?response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD; Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found

AA exchange(s) at position (first base of changed triplet):
139(1eu->met) 166(1le->val)
Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES

source

1..852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834G1127D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
1..852
/gene="MTAP"
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/gene="MTAP"
/codon_start=1
/protein_id="GI:49456301"
/db_xref="GI:49456301"
/translation="MASGTTTAVKIGIIGGTGLDDEILBGRTEKYVDTPFGKPSDA
LIMGKIKNVDCVLLARHGRQHTIMPSKVNQANIMWLKEEGCTHVITTAAGSLREI
QPGDIVIIDQFIDRTTMRPQSFYDGSWSCARGVCHIPMAEPFCPKTREVLLETAKKLG
LRCHSKGTWVITIEGPRSSRAESFMRTWGADVIMNTVPEVVLAKKAGICVASIAMA
TDYDCWKEHEBAVSVDRLVLTLEKANKAKSLLLTTIPQIGSTWSETLHNLKMAQF
SVLLPRH"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
|||||
Db 691 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 750
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 120
|||||
Db 751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 810
QY 121 AAG 123
|||
Db 811 AAG 813

RESULT 7
AX826996 870 bp DNA linear PAT 12-DEC-2003

LOCUS AX826996

DEFINITION Sequence 1 from Patent WO03074083.

ACCESSION AX826996

VERSION AX826996.1 GI:39837205

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Bloom, L.A., Boritzki, T.J., Kung, P.P., Ogden, R.C., Skalitzy, D.J.,

TITLE Zehnder, L.R., Kuhn, L.A. and Meng, J.J.

JOURNAL Combination therapies for treating methylthioadenosine

phosphorylase deficient cells

PATENT: WO 03074083-A 1 12-SEP-2003;

PFIZER INC. (US)

FEATURES

source

1..870
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Cloned MTAP cDNA"

ORIGIN

QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
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Db 697 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 756

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 120
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Db 757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 816

QY 121 AAG 123
|||

Db 817 AAG 819

RESULT 8

LOCUS L40432

DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,

complete cds.

ACCESSION L40432

VERSION L40432.1 GI:11602391

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Batova, A., Yu, A.L.

JOURNAL and Carson, D.A.

REFERENCE Genomic cloning of methylthioadenosine phosphorylase: a purine

MEDLINE metabolic enzyme deficient in multiple different cancers

PUBMED Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)

AUTHORS 96234115

TITLE 8650244

JOURNAL 2 (bases 1 to 1021)

COMMENT Nobori, T., Takabayashi, K., Tran, P., Orvis, L., Batova, A., Yu, A.L.

FEATURES and Carson, D.A.

source

1..1021

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="9"

/map="9p22-p21"

/tissue type="placenta"

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/gene="MTAP"

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/protein_id="AA038871.1"

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LIMGKIKNVDCVLLARHGRQHTIMPSKVNQANIMWLKEEGCTHVITTAAGSLREI

QPGDIVIIDQFIDRTTMRPQSFYDGSWSCARGVCHIPMAEPFCPKTREVLLETAKKLG

LRCHSKGTWVITIEGPRSSRAESFMRTWGADVIMNTVPEVVLAKKAGICVASIAMG

TDYDCWKEHEBAVSVDRLVLTLEKANKAKSLLLTTIPQIGSTWSETLHNLKMAQF

SVLLPRH"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 1021;

Best Local Similarity 100.0%; Pred. No. 1.5e-28;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60

|||||

Db 697 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 756

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 120

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Db 751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCCATAACCTG 810

QY 121 AAG 123

|||

Db 811 AAG 813

RESULT 7

AX826996 870 bp DNA linear PAT 12-DEC-2003

LOCUS AX826996

DEFINITION Sequence 1 from Patent WO03074083.

ACCESSION AX826996

VERSION AX826996.1 GI:39837205

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Bloom, L.A., Boritzki, T.J., Kung, P.P., Ogden, R.C., Skalitzy, D.J.,

TITLE Zehnder, L.R., Kuhn, L.A. and Meng, J.J.

JOURNAL Combination therapies for treating methylthioadenosine

phosphorylase deficient cells

PATENT: WO 03074083-A 1 12-SEP-2003;

PFIZER INC. (US)

FEATURES

source

1..870
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Cloned MTAP cDNA"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 1021;

Best Local Similarity 100.0%; Pred. No. 1.5e-28;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATTAAGCCCAAAAGCTTA 60
|||||
Db 801 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATTAAGCCCAAAAGCTTA 860
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||||
Db 861 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 920
QY 121 AAG 123
|||
Db 921 AAG 923
RESULT 9
LOCUS BC026106 1890 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens methylthioadenosine phosphorylase, mRNA (CDNA clone
MGC:33067 IMAGE:4820938), complete cds.
ACCESSION BC026106
VERSION BC026106.1 GI:19913486
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1890)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1890)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2002) National Institutes of Health, Mammalian
PUBMED Gene Collection (MGC), Cancer Genomics Office, National Cancer
REFERENCE Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
TITLE NIH-MGC Project URL: http://mgc.nci.nih.gov
JOURNAL Contact: MGC help desk
PUBMED Email: cgabs-r@mail.nih.gov
REFERENCE Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
AUTHORS cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
REMARK
COMMENT
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 46 Row: h Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6006025.

FEATURES
source
location/Qualifiers
1..1890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:33067 IMAGE:4820938"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"
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/gene="MTAP"
/note="synonyms: MSAP, c86fus"
/db_xref="LOCUSID:4507"
/db_xref="MIM:156540"
96..947
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/product="5'-methylthioadenosine phosphorylase"
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/db_xref="GI:19913487"
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LILGKIKNVDCILARHGRQHTIMPISKVNYQANIMALKEGCTHIVITACGSLREI
QPGDIVIIDQIDRTTMRPQSFYDGSHCARGVCHI PMAEFPCKTREVLIETAKLG
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TDYDCWKEHEEAVSDRVILKTKENANKAKSLLTITPIQIGSTWSETHNLKNAQF
SVLLPRH"
ORIGIN
Query Match 100.0%; Score 123; DB 9; Length 1890;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATTAAGCCCAAAAGCTTA 60
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Db 786 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATTAAGCCCAAAAGCTTA 845
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||||
Db 846 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 905
QY 121 AAG 123
|||
Db 906 AAG 908
RESULT 10
LOCUS HSU22233 2269 bp mRNA linear PRI 25-NOV-1995
DEFINITION Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.
ACCESSION U22233
VERSION U22233.1 GI:847723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2269)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Olopade,O.I., Pomyskala,H.M., Hagos,F., Sween,L.W., Espinosa,R. III,
Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and
Bohlender,S.K.
Construction of a 2.8-megabase yeast artificial chromosome contig
and cloning of the human methylthioadenosine phosphorylase gene
from the tumor suppressor region on 9p21
Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
95327672
JOURNAL MEDLINE
PUBMED 7604019
REFERENCE 2 (bases 1 to 2269)
AUTHORS Olopade,O.I.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,

University of Chicago Pritzker School of Medicine, 5841 S. Maryland Avenue, Chicago, IL 60637-1470, USA

FEATURES
source

1. .2269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"
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/sex="male"
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/cell_type="fibroblast"
/tissue_type="epidermis"
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122. .973
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SVLLPRH"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 2269;
Best Local Similarity 100.0%; Pred. No. 1.5e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 812 GTTTCGGTGGACCGGGTCTTAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 871
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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Db 872 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 931
QY 121 AAG 123
|||
Db 932 AAG 934

RESULT 11
AR059583 2763 bp DNA linear PAT 29-SEP-1999
LOCUS AR059583
DEFINITION Sequence 1 from patent US 5840505.
ACCESSION AR059583
VERSION AR059583.1 GI:5986033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
TITLE Method for inhibiting adenylosuccinate synthetase activity in
JOURNAL Patent: US 5840505-A 1 24-NOV-1998;
FEATURES
source location/Qualifiers
1. .2763
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 60

|||||
Db 1640 GTTTCGGTGGACCGGGTCTTAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 1699

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759

QY 121 AAG 123
|||
Db 1760 AAG 1762

RESULT 12

LOCUS 128320 2763 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5571510.
ACCESSION 128320
VERSION 128320.1 GI:1819096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Nobori,T. and Carson,D.A.
TITLE Method for selective methionine starvation of malignant cells in
JOURNAL Patent: US 5571510-A 1 05-NOV-1996;
FEATURES
source location/Qualifiers
1. .2763
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||||
Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759
QY 121 AAG 123
|||
Db 1760 AAG 1762

RESULT 13
AR473576 2763 bp DNA linear PAT 20-FEB-2004
LOCUS AR473576
DEFINITION Sequence 14 from patent US 6689561.
ACCESSION AR473576
VERSION AR473576.1 GI:42711901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Tumor suppressor gene and methods for detection of cancer,
JOURNAL Patent: US 6689561-A 14 10-FEB-2004;
FEATURES
source location/Qualifiers
1. .2763
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 60
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QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 120
1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 1759

QY 121 AAG 123
1760 AAG 1762

Db

RESULT 14
AR474046 2763 bp DNA linear PAT 20-FEB-2004
LOCUS AR474046
DEFINITION Sequence 14 from patent US 6689864.
ACCESSION AR474046
VERSION AR474046.1 GI:42712799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Cyclin dependent kinase 4 inhibitor
JOURNAL Patent: US 6689864-A 14 10-FEB-2004;
FEATURES Location/Qualifiers
source 1..2763
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 60
1640 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 1699

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 120
1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 1759

QY 121 AAG 123
1760 AAG 1762

Db

RESULT 15
AR144466 3083 bp DNA linear PAT 08-AUG-2001
LOCUS AR144466
DEFINITION Sequence 1 from patent US 6210917.
ACCESSION AR144466
VERSION AR144466.1 GI:15106333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3083)
AUTHORS Carson,D.A. and Carrera,C.J.
TITLE Method for suppressing multiple drug resistance in cancer cells
JOURNAL Patent: US 6210917-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..3083
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 3083;

Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 60
2426 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 2485

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 120
2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTAGAAAACCTCCATAACCTG 2545

QY 121 AAG 123
2546 AAG 2548

Db

Search completed: February 1, 2005, 13:26:00
Job time : 693.095 secs

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 161.422 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGACCGGCTCTT.....AAACCTCCATTAACCTGAAG 123

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	870	10 ADC37133	Adc37133 Cloned me
2	123	100.0	2197	10 ADC30327	Adc30327 Human nov
3	123	100.0	2763	2 AAT15167	Aat15167 Methylthi
4	123	100.0	2763	2 AAQ92813	Aaq92813 Human MTA
5	123	100.0	2763	2 AAT85305	Aat85305 Human met
6	123	100.0	2763	2 AAZ00866	Aaz00866 Human MTA
7	123	100.0	2763	5 AAF86091	Aaf86091 Methylthi
8	123	100.0	2763	10 AAD64097	Aad64097 Human met
9	123	100.0	2784	2 AAQ99202	Aaq99202 Pseudomon
10	123	100.0	3083	2 AAX58284	Aax58284 Human met
11	123	100.0	3083	4 ABX10818	Abx10818 DNA encod
12	113	91.9	1437	4 AAH33683	Aah33683 Human col
13	41.2	33.5	662	6 ABQ59125	Abq59125 Human col
14	31.2	25.4	603	6 ABQ59540	Abq59540 Human col
15	31	25.2	145831	6 ABL69213	Ab169213 Prostate
16	31	25.2	145831	6 ABL66806	Ab166806 Lung canc
17	31	25.2	145831	6 ABL68588	Ab168588 Kidney ca
18	31	25.2	145831	6 ABL62309	Ab162309 Colon ade
19	31	25.2	145831	6 ABL10149	Abt10149 Human bre
20	29.8	24.2	760	6 ABQ16984	Abq16984 Oligonuc1
21	29.8	24.2	760	6 ABQ16985	Abq16985 Oligonuc1

C	22	29.8	24.2	61557	4 AAS59521	Aas59521 Propionib
C	23	29.8	24.2	61557	8 ACf64450	Acf64450 Propionib
C	24	29.2	23.7	2207	10 ADD89080	Add89080 Encoding
C	25	29.2	23.7	2207	12 ADL91576	Adl91576 Human imm
C	26	29.2	23.7	2213	8 ABZ35866	Abz35866 Human sec
C	27	29.2	23.7	3103	8 ABZ36155	Abz36155 Human sec
C	28	29.2	23.7	6815	11 ADL22655	Adl22655 Human dis
C	29	29	23.6	7746	6 ABK40047	Abk40047 Human che
C	30	29	23.6	7746	6 ABJ33856	Abj33856 Human imm
C	31	28.8	23.4	2891	10 ADH54930	Adh54930 Human ins
C	32	28.4	23.1	14112	4 AAS46477	Aas46477 Tumour su
C	33	28.4	23.1	14112	6 ABJ33442	Abj33442 Human imm
C	34	28.4	23.1	14112	6 ABK31332	Abk31332 Signal tr
C	35	28.4	23.1	14112	6 ABQ66979	Abq66979 Human ang
C	36	28.2	22.9	6098	6 ABL32519	Ab132519 Human imm
C	37	28.2	22.9	9258	4 ABL12730	Ab112730 Drosophill
C	38	28.2	22.9	17077	10 ADD48825	Add48825 Human gen
C	39	28.2	22.9	24419	4 ABL10682	Ab110682 Drosophill
C	40	28.2	22.9	24419	4 ABL18670	Ab118670 Tumour su
C	41	28.2	22.9	61020	4 AAS46788	Aas46788 Tumour su
C	42	28	22.8	223	9 ADA09632	Ada09632 Restricti
C	43	28	22.8	419	5 ABV10652	Abv10652 Human pro
C	44	28	22.8	1794	3 AAA30256	Aaa30256 Rat patri
C	45	28	22.8	2286	12 ADI81563	Adi81563 Rat stret

ALIGNMENTS

RESULT 1	
ID	ADC37133
ID	ADC37133 standard; cDNA, 870 BP.
XX	
AC	ADC37133;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Cloned methylthiadenosine phosphorylase, MTAP, cDNA.
XX	
KW	combination therapy; methylthiadenosine phosphorylase; MTAP; inhibitor;
KW	glycinamide ribonucleotide formyltransferase; GARFT;
KW	aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW	anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW	glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW	pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX	
OS	Unidentified.
XX	
PN	WO2003074083-A1.
XX	
PD	12-SEP-2003.
XX	
PF	17-FEB-2003; 2003WO-IB000615.
XX	
PR	04-MAR-2002; 2002US-0361645P.
PR	09-DEC-2002; 2002US-0432275P.
XX	
PA	(PFIZ) PFIZER INC.
XX	
PI	Bloom LA, Boritzki TJ, Kung P, Ogden RC, Skallitzky DJ;
PI	Zehnder LR, Kuhn LA, Meng JJ;
XX	
DR	WPI; 2003-748252/70.
XX	
PT	Selectively killing methylthiadenosine phosphorylase deficient cells
PT	used for treating cell proliferative disorders comprises administering
PT	glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX	
PS	Example 3B; Page 182-183; 189pp; English.
XX	
CC	This invention relates to novel combination therapies that selectively
CC	kill methylthiadenosine phosphorylase (MTAP) deficient cells. The
CC	combination therapies comprise administering an inhibitor of glycinamide

CC ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC toxicity agent during and after administration of the inhibitor. The
CC combination therapies can be used for selectively killing MTAP deficient
CC cells, and for treating cell proliferative disorders e.g. lung cancer,
CC leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC dose of the inhibitor. This polynucleotide sequence represents the cloned
CC MTAP cDNA of the invention.
XX
SQ Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 123; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 60
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Db 697 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 756
|||
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTGAGAAACCTCCATAACCTG 120
|||
Db 757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTGTGAGAAACCTCCATAACCTG 816
|||
QY 121 AAG 123
|||
Db 817 AAG 819

RESULT 2
ADC30327 ID ADC30327 standard; cDNA; 2197 BP.
XX
AC ADC30327;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:409.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 3; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI; 2003-371981/35.
DR P-PSDB; ADC31298.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.

XX Claim 1; SEQ ID NO 409; 1185bp; English.
PS
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Match 100.0%; Score 123; DB 10; Length 2197;
Best Local Similarity 100.0%; Pred. No. 2.1e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 60
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Db 751 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 810
|||
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTGTGAGAAACCTCCATAACCTG 120
|||
Db 811 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTGTGAGAAACCTCCATAACCTG 870
|||
QY 121 AAG 123
|||
Db 871 AAG 873

RESULT 3
AAT15167 ID AAT15167 standard; DNA; 2763 BP.
XX
AC AAT15167;
XX
DT 29-JUN-1996 (first entry)
XX
DE Methylthioadenosine-phosphorylase gene.
XX
KW Human; methylthioadenosine-phosphorylase; chromosome walking;
KW interferon-alpha; CDK41; tumour suppressor; chromosome-9p21;
KW cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW antibody; imaging; ss.
XX
OS Homo sapiens.

```
XX Key Location/Qualifiers
FH exon 254..421
FT exon /*tag= b
FT intron 422..615
FT exon /*tag= c
FT exon 616..720
FT intron /*tag= d
FT intron 721..963
FT exon /*tag= e
FT exon 964..1203
FT exon /*tag= f
XX WO9528169-A1.
XX 26-OCT-1995.
XX 12-APR-1995; 95WO-US004655.
XX 14-APR-1994; 94US-00227800.
XX (REGC ) UNIV CALIFORNIA.
XX PA
XX PI Carson DA, Nobori T;
XX DR WPI; 1995-373630/48.
XX PT Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
XX PT useful for diagnosis, assessing predisposition and treatment of cancers.
XX PS Example 1; Page 96-101; 129pp; English.
XX CC The sequence encodes a methylthioadenosine-phosphorylase, and is located
XX CC at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
XX CC tumour suppressor gene (AAT15157-58) is located between this gene and an
XX CC interferon-alpha gene cluster, and has been isolated by chromosome
XX CC walking. The CDK4I gene, probe and primer derivatives and the gene
XX CC product may be used in diagnosis of cancer, particularly melanoma
XX CC (especially dysplastic nevus syndrome), glioma, non-small cell lung
XX CC carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
XX CC or in antitumour antisense oligonucleotide or ribozyme construction.
XX CC Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;
Query Match 100.0%; Score 123; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTTCGGTGGACCGGGTCTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
DB 1640 GTTTCGGTGGACCGGGTCTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699
OY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 120
DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 1759
OY 121 AAG 123
DB 1760 AAG 1762
RESULT 4
AAQ92813
ID AAQ92813 standard; DNA; 2763 BP.
XX
XX AAQ92813;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-DEC-1995 (first entry)
XX
XX Human MTase.
XX
```

```
KW MTase; methyladenosine-phosphatase; malignancy; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH exon 254..421
FT exon /*tag= a
FT exon 616..720
FT exon /*tag= b
FT exon 964..1203
FT exon /*tag= c
FT exon 1640..1762
FT exon /*tag= d
FT exon 2272..2310
FT exon /*tag= e
XX WO9518233-A1.
XX 06-JUL-1995.
XX 22-DEC-1994; 94WO-US014920.
XX 29-DEC-1993; 93US-00176855.
XX (REGC ) UNIV CALIFORNIA.
XX PA (CIBA ) CIBA GEIGY CORP.
XX PI Nobori T, Carson DA, Takabayashi K;
XX DR WPI; 1995-246398/32.
XX PT Detecting methyl:adenosine phosphatase in mammalian cells - by
XX PT hybridisation with specific oligonucleotide for detecting malignancy,
XX PT also new nucleic acid, expression vectors, derived polypeptide(s) and
XX PT antibodies.
XX PS Claim 8; Page 34-35; 47pp; English.
XX CC A cosmid gene library constructed from human placenta DNA was screened
XX CC using a MTase cDNA probe to isolate a human MTase genomic clone (sequence
XX CC given in AAQ92813). Absence of MTase from a cell is indicative of
XX CC malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;
```

```
Query Match 100.0%; Score 123; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTTCGGTGGACCGGGTCTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
DB 1640 GTTTCGGTGGACCGGGTCTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699
OY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 120
DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 1759
OY 121 AAG 123
DB 1760 AAG 1762
RESULT 5
AAT85305
ID AAT85305 standard; DNA; 2763 BP.
XX
XX AAT85305;
AC
XX
XX 28-FEB-1998 (first entry)
DT Human methylthioadenosine phosphorylase.
XX
XX Human methylthioadenosine phosphorylase; MTase; human;
KW
```

KW adenylsuccinate synthetase; lung cancer; glioma;
KM acute lymphoblastic leukaemia; urothelial tumour; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 254..421
FT /*tag= a
FT /number= 1
FT intron 422..615
FT /*tag= b
FT /number= 1
FT exon 616..720
FT /*tag= c
FT /number= 2
FT intron 721..963
FT /*tag= d
FT /number= 2
FT exon 964..1203
FT /*tag= e
FT /number= 3
XX
XX WO9732994-A1.
XX
XX 12-SEP-1997.
XX
XX 27-JAN-1997; 97WO-US001193.
XX
XX 08-MAR-1996; 96US-00612542.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
XX WPI; 1997-470550/43.
XX
XX Inhibiting adeny1:succinate synthetase activity in methylthio:adenosine
PT phosphorylase-deficient cells - by treatment with specific inhibitor,
PT especially L-alanosine, useful for selective killing of MTase deficient
PT cancer cells.
XX
XX
PS Example 3; Page 25-26; 37pp; English.
XX
XX This DNA sequence comprises human genomic DNA for methylthioadenosine
CC phosphorylase (MTase), obtained from a cosmid gene library constructed
CC from human placenta DNA by screening with a MTase cDNA probe. A claimed
CC method for inhibiting the activity adeny1succinate synthetase (ASS) in
CC mammalian cells deficient in MTase activity involves: (a) determining
CC that a population of cells obtained from a mammalian host is MTase
CC deficient; and (b) administering an ASS inhibitor (preferably L-
CC alanosine) to the host so that the MTase deficient host cells are
CC depleted of AMP. The method is especially used to treat human MTase-
CC deficient primary tumour cells, specifically non-small cell lung cancer,
CC acute lymphoblastic leukaemia (ALL), glioma and urothelial tumour cells.
CC MTase catabolises methylthioadenosine to adenine for endogenous salvage
CC incorporation into the intracellular AMP pool. The claimed method
CC deprives the cells of substrate for de novo synthesis of AMP, resulting
CC in selective killing of these cells. MTase sequence-specific
CC oligonucleotides can be used to detect the presence or absence of MTase in
CC malignant cell lines
XX
SQ Sequence 2763 BP; 780 A; 505 C; 597 G; 804 T; 0 U; 77 Other;

Query Match 100.0%; Score 123; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGGTCTTAAGAACCCTGAAGAAACGCTAATAAGCCAAAAGCTTA 60
|||
Db 1640 GTTTCGGTGAACCGGGTCTTAAGAACCCTGAAGAAACGCTAATAAGCCAAAAGCTTA 1699
|||
QY 61 CTGCTCACTACATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTTCATACCTG 120
|||

Db 1700 CTGCTCACTACATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTTCATACCTG 1759
QY 121 AAG 123
|||
Db 1760 AAG 1762

RESULT 6
AAZ00866
ID AAZ00866 standard; DNA; 2763 BP.
XX
XX AAZ00866;
AC
XX 20-OCT-1999 (first entry)
DT
XX
XX Human MTase DNA.
DE
XX
XX MTase; methylthioadenosine phosphorylase; human; detection; active;
KW catalytic; malignant cell; methionine starvation therapy; ss.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT exon 253..421
FT /*tag= a
FT /number= 1
FT intron 422..615
FT /*tag= b
FT /number= 1
FT /note= "putative intron"
FT exon 616..720
FT /*tag= c
FT /number= 2
FT /note= "putative exon"
FT intron 721..963
FT /*tag= d
FT /number= 2
FT /note= "putative intron"
FT exon 964..1203
FT /*tag= e
FT /number= 3
FT /note= "putative exon"
XX
XX US5942393-A.
XX
XX 24-AUG-1999.
XX
XX 18-DEC-1996; 96US-00772113.
XX
XX 29-DEC-1993; 93US-00176855.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Takabayashi K, Carson DA, Nobori T;
XX
XX WPI; 1999-507775/42.
XX
XX
PT Detecting catalytically active and inactive methylthioadenosine
PT phosphorylase (MTase) in mammalian cells useful for identifying malignant
PT cells which are suitable targets for methionine (MET) starvation therapy.
XX
XX
PS Claim 6; Fig 1; 14pp; English.
XX
XX This invention describes a novel method for detecting catalytically
CC active and inactive methylthioadenosine phosphorylase (MTase) in
CC mammalian cells, using oligonucleotide probes which hybridize to MTase
CC nucleic acid coding regions. Detection of MTase encoding nucleic acid
CC indicates the cell has catalytically active MTase. The method is useful
CC for detecting malignant cells with a deficient MTase gene, useful for
CC identifying malignant cells which are suitable targets for methionine
CC (MET) starvation therapy. The new method is simple, efficient and
CC successful at determining MTase negative cells, unlike prior art

CC techniques, which include analysis of catalytic activity in cell
CC cultures, requiring a commercially unavailable radiochemical substrate,
CC and immunoassays, using MTase antibodies which are unable to be produced
CC in sufficient quantities. Recombinant MTase protein produced using the
CC new polynucleotide and vector, allows greater and purer production of
CC MTase than prior art techniques (using the Rangione method) for isolating
CC native MTase. This sequence represents human MTase encoding DNA which is
CC used in the method of the invention

XX Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

QY Query Match 100.0%; Score 123; DB 2; Length 2763;

Best Local Similarity 100.0%; Pred. No. 2.3e-33;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GTTTCGGTGACCGGGTCTTAAGACCGCTGAAGAAACGCTAATAAGCCAAAGCTTA 60
1640 GTTTCGGTGACCGGGTCTTAAGACCGCTGAAGAAACGCTAATAAGCCAAAGCTTA 1699

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759

QY 121 AAG 123
Db 1760 AAG 1762

RESULT 7
AAF86091
ID AAF86091 standard; DNA; 2763 BP.
XX AAF86091;
AC
XX 06-JUL-2001 (first entry)
DT
XX Methylothiadenosine phosphorylase.
DE
XX Methylothiadenosine phosphorylase; adenyl succinate synthetase; ASS;
KW cancer; ds.
XX Unidentified.
OS
XX US6214571-B1.
PN
XX 10-APR-2001.
PD
XX 24-NOV-1998; 98US-00199137.
PF
XX 29-DEC-1993; 93US-00176855.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Carrera CJ, Carson DA, Cottam HB, Nobori T;
PI
XX WPI; 2001-315458/33.
DR
XX Inhibiting adenine succinate synthetase (ASS) activity in
PT methylothiadenosine phosphorylase deficient cells of mammalian host
PT involves administering ASS inhibitor which depletes adenosine 5'
PT monophosphate in cells.
XX
XX Disclosure; Fig 1; 17pp; English.
PS
XX The present invention relates to inhibiting adenyl succinate synthetase
CC (ASS) activity in methylothiadenosine phosphorylase (MTase) deficient
CC cells of mammalian host. The invention may be used as a treatment for
CC cancer, especially breast and colon cancer
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 123; DB 5; Length 2763;

Best Local Similarity 100.0%; Pred. No. 2.3e-33;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAGACCGCTGAAGAAACGCTAATAAGCCAAAGCTTA 60
Db 1640 GTTTCGGTGACCGGGTCTTAAGACCGCTGAAGAAACGCTAATAAGCCAAAGCTTA 1699

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759

QY 121 AAG 123
Db 1760 AAG 1762

RESULT 8
AAD64097
ID AAD64097 standard; DNA; 2763 BP.
XX AAD64097;
AC
XX 12-FEB-2004 (first entry)
DT
XX Human methylothiadenosine phosphorylase (MTase) genomic DNA.
DE
XX Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylothiadenosine phosphorylase; MTase;
KW ds.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH exon 254..421
FT exon /*tag= a
FT intron 422..615
FT exon /*tag= b
FT exon 616..720
FT intron /*tag= c
FT intron 721..963
FT exon /*tag= d
FT exon 964..1203
FT exon /*tag= e

US2003138928-A1.

24-JUL-2003.

18-JUL-2001; 2001US-00908671.

26-AUG-1997; 97US-00921954.

(CARS/) CARSON D A.
(NOBO/) NOBORI T.

Carson DA, Nobori T;

WPI; 2003-851737/79.

New isolated polynucleotide encoding cyclin-dependent kinase 41, useful
for preparing a composition for diagnosing or treating cancer.

Example 1; SEQ ID NO 14; 46pp; English.

XX The present invention relates to novel tumour suppressor genes, termed as
CC cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC proteins. The polynucleotides are useful for preparing a composition for
CC diagnosing or treating cancer. Sequences of the invention are also useful
CC in gene therapy. The present sequence is human methylothiadenosine
CC phosphorylase (MTase) genomic DNA used in the exemplification of the
CC invention

Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 123; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTCGGTGACCGGCTTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
Db 1640 GTTTCGGTGACCGGCTTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAAACCCCTCATAACTTG 120
Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAAACCCCTCATAACTTG 1759
QY 121 AAG 123
Db 1760 AAG 1762

RESULT 9
AAQ99202
ID AAQ99202 standard; DNA; 2784 BP.
AC AAQ99202;
XX
DT 07-MAR-1996 (first entry)
XX
DE Pseudomonas putida methylthiodenosine-phosphorylase DNA.
XX
KW Enzyme; MTase; L-Met-L-deamino-gamma-mercaptopmethane-lyase;
KW chemotherapy; cancer therapy; methionine starvation; ss.
XX
OS Pseudomonas putida.
XX
FH Key Location/Qualifiers
FT CDS 1..2763
FT /*tag= a
XX
PN WO9517908-A1.
XX
PD 06-JUL-1995.
XX
PF 22-DEC-1994; 94WO-US014919.
XX
PR 29-DEC-1993; 93US-00176413.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Nobori T, Carson DA;
XX
XX WPI; 1995-246192/32.
DR
XX
PT Selective methionine starvation of methyl:thio:adenosine phosphorylase
PT negative tumour cells - used in chemotherapy of mammalian malignant
PT cells.
XX
PS Disclosure; Page 27-28; 46pp; English.
XX
CC Antigenic peptides may be generated from this sequence encoding
CC methyladenosine-phosphorylase, which are then used to generate antibodies
CC specific for MTase. The produced antibodies may be used in an immunoassay
CC for the detection of MTase
XX
SQ Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

Query Match 100.0%; Score 123; DB 2; Length 2784;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGCTTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
Db 1640 GTTTCGGTGACCGGCTTTAAGACCCCTGAAGAAAACGCTAATAAAGCCAAAAGCTTA 1699
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAAACCCCTCATAACTTG 120

Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGGTCAGAAAACCCCTCATAACTTG 1759
QY 121 AAG 123
Db 1760 AAG 1762

RESULT 10
AAX58284
ID AAX58284 standard; DNA; 3083 BP.
XX
AC AAX58284;
XX
DT 02-AUG-1999 (first entry)
XX
DE Human methylthiodenosine phosphorylase genomic DNA.
XX
KW Methylthiodenosine phosphorylase; MTase; human;
KW multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW therapy; ss.
XX
OS Homo sapiens.

Location/Qualifiers
119..2876

/*tag= a
/note= "contains introns"

119..151

/*tag= b
/number= 1

152..449

/*tag= c
/number= 1

450..536

/*tag= d
/number= 2

537..723

/*tag= e
/number= 2

724..782

/*tag= f
/number= 3

783..898

/*tag= g
/number= 3

899..1067

/*tag= h
/number= 4

1068..1377

/*tag= i
/number= 4

1378..1480

/*tag= j
/number= 5

1481..1763

/*tag= k
/number= 5

1764..1953

/*tag= l
/number= 6

1954..2425

/*tag= m
/number= 6

2426..2548

/*tag= n
/number= 7

2549..2837

/*tag= o
/number= 7

2838..2876

/*tag= p
/number= 8

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PN WO9920791-A1.
XX
PD 29-APR-1999.
XX
PF 23-OCT-1998; 98WO-US022557.
XX
PR 23-OCT-1997; 97US-00956657.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Carson DA, Cottam HB, Nobori T, Carrera CJ;
XX
DR WPI; 1999-302753/25.
XX
PT Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT leukemia's.
PS
XX Example 3; Page 42-44; 45pp; English.
XX
CC This is the DNA sequence of a human methylthioadenosine phosphorylase
CC (MTase) genomic DNA clone that was isolated from a cosmid gene library
CC using an MTase cDNA probe. The encoded enzyme catabolises
CC methylthioadenosine to adenine for endogenous salvage incorporation into
CC the intracellular AMP pool. The invention relates to methods for treating
CC and preventing the onset and maintenance of multiple drug resistance
CC (MDR) in animals undergoing cancer chemotherapy. In the methods provided,
CC cells are depleted of AMP and ATP and are thus unable to support P-
CC glycoprotein activity. One method obtains a population of target cells
CC from a host and assays for loss of MTase activity. MTase deficient cells
CC are treated with a purine synthesis inhibitor, such as L-alanosine, which
CC starves the cells of adenine and suppresses P-glycoprotein activity. The
CC MTase deficient host cells are preferably primary tumour cells comprising
CC small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma
CC cells or urothelial tumor cells, preferably in humans. MTase competent
CC cells are also treated for MDR with purine synthesis inhibitors. MTase
CC competent and deficient cells are also treated for malignancy with other
CC anti-cancer drugs. MTase sequence-specific oligonucleotides can be used
CC to detect the presence or absence of MTase in malignant cell lines
CC
XX
SQ Sequence 3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;
XX
Query Match 100.0%; Score 123; DB 2; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
DB 2426 GTTTCGGTGGACCGGGTCTTAAAGACCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 24855
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATTAACCTG 120
DB 2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATTAACCTG 25455
QY 121 AAG 123
DB 2546 AAG 2548
XX
RESULT 11
ABX10818
ID ABX10818 standard; DNA; 3083 BP.
XX
AC ABX10818;
XX
DT 17-APR-2003 (first entry)
XX
DE DNA encoding rat methylthioadenosine phosphorylase (MTase).
XX
KM Rat; methylthioadenosine phosphorylase; MTase; detection;
XX
KW Rangelone method; gene; ds.
XX
OS Rattus sp.
XX

```

Key	Location/Qualifiers
FT exon	119. .151
FT	/tag= a
FT	/number= 1
FT intron	152. .449
FT	/tag= b
FT	/number= 1
FT exon	450. .536
FT	/tag= a
FT	/number= 2
FT intron	537. .723
FT	/tag= b
FT	/number= 2
FT exon	724. .782
FT	/tag= a
FT	/number= 3
FT intron	783. .898
FT	/tag= b
FT	/number= 3
FT exon	899. .1066
FT	/tag= a
FT	/number= 4
FT intron	1067. .1377
FT	/tag= b
FT	/number= 4
FT exon	1378. .1480
FT	/tag= a
FT	/number= 5
FT intron	1481. .1763
FT	/tag= b
FT	/number= 5
FT exon	1764. .1953
FT	/tag= a
FT	/number= 6
FT intron	1954. .2425
FT	/tag= b
FT	/number= 6
FT exon	2426. .2548
FT	/tag= a
FT	/number= 7
FT intron	2549. .2837
FT	/tag= b
FT	/number= 7
FT exon	2838. .2876
FT	/tag= a
FT	/number= 8
XX	US2002146695-A1.
XX	
XX	10-OCT-2002.
XX	
XX	09-FEB-2001; 2001US-00780114.
XX	
XX	29-DEC-1993; 93US-00176855.
XX	02-JUN-1995; 95US-00459343.
XX	04-MAY-1998; 98US-00072914.
XX	
XX	(NOBO/) NOBORI T.
XX	(CARSON/) CARSON D A.
XX	(TAKA/) TAKABAYASHI K.
XX	
XX	Nobori T, Carson DA, Takabayashi K;
XX	
XX	WPI; 2003-208976/20.
XX	
XX	Detection of methylthioadenosine phosphorylase presence in mammalian
XX	cells, by adding to sample oligonucleotide probes capable of hybridizing
XX	to methylthioadenosine phosphorylase encoding nucleic acid.
XX	
XX	Claim 7; Fig 1; 16pp; English.
XX	
XX	The invention describes a method of detecting methylthioadenosine
XX	phosphorylase (MTase) comprising adding oligonucleotide probes
XX	

CC hybridisable to MTase encoding nucleic acid to an assayable sample of
CC cells, where the presence of the nucleic acid indicates the presence of
CC the MTase in a cell. The inventive method is simple and efficient in
CC detecting the presence of MTase in the mammalian cell. The availability
CC of the recombinant MTase enables the production of highly pure material
CC with greater ease and in greater quantities than was obtained using
CC Rangione method for the isolation and purification of native MTase. This
CC sequence encodes rat methylthiodenosine phosphorylase (MTase)
XX
SQ Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

Query Match 100.0%; Score 123; DB 8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 60
Db 2426 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTA 2485
Oy 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAAACCCCTCATTAACCTG 120
Db 2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAAACCCCTCATTAACCTG 2545
Oy 121 AAG 123
Db 2546 AAG 2548

RESULT 12

AAH33683
ID ID AAH33683 standard; cDNA; 1437 BP.

AC AAH33683;
DT 03-SEP-2001 (first entry)

DE Human colon cancer antigen encoding cDNA SEQ ID NO:739.

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 9; ss.

OS Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

PR 29-SEP-1999; 99US-0157137P.

PR 03-NOV-1999; 99US-0163280P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI; 2001-235357/24.

DR P-PSDB; AAG74252.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.

PS Claim 1; Page 2728-2729; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to

CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 1437 BP; 501 A; 202 C; 262 G; 460 T; 0 U; 12 Other;

Query Match 91.9%; Score 113; DB 4; Length 1437;
Best Local Similarity 95.0%; Pred. No. 6.9e-30;
Matches 113; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CGGTGACCGGGTCTTAAAGACCCCTGAAAGAAAACGCTAATAAAGCCAAAAGCTTAAGTGC 64
Db 1 CGGTGTACCGTGTCTTAAAGCCCTGAAAGAAWAAACGCTAATAAAMGCCAAAAGCTTAAGTGC 60
Oy 65 TCACCTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAAACCCCTCATTAACCTGAAG 123
Db 61 TCACCTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAAACCCCTCMTAAGCTGAAG 119

RESULT 13

ABQ59125
ID ID ABQ59125 standard; cDNA; 662 BP.

AC ABQ59125;

DT 02-AUG-2002 (first entry)

DE Human colon cancer related nucleotide sequence SEQ ID NO:2820.

KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.

OS Homo sapiens.

PN WO200229086-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US030732.

PR 02-OCT-2000; 2000US-0237271P.

PA (FARB) BAYER CORP.

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;

PI Thiaglingam A, Lewis ME;

DR WPI; 2002-426115/45.

PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.

PS Claim 1; Fig 1; 796pp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate

CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists

XX
SQ Sequence 662 BP; 171 A; 134 C; 148 G; 165 T; 0 U; 44 Other;

Query Match 33.5%; Score 41.2; DB 6; Length 662;
Best Local Similarity 71.3%; Pred. No. 0.00023;
Matches 87; Conservative 0; Mismatches 30; Indels 5; Gaps 3;

QY 2 TTTCGGTGGACCGGCTCTTAAGACCTGAAG--AAAACGCTAATAAGCCA-AAAGCT 58
Db ||||| 444 TTCCGGTGGACCGGCTTTAAANGCCTGGAGAAAGAAACCGCTTTTAAANCCATAAAGCT 503

QY 59 TACTGCTCACTACCA--TACCTCAGATAGGGTCCACAGATGTCAGAAACCTCCATAA 116
Db ||||| 504 TANTGNTCNATTACAATACCTNNAGATAGGGTCNACAAATGCTCCANAAAAACCTCNTAA 563

QY 117 CC 118
AC ||
Db 564 CC 565

RESULT 14
ABQ59540/C
ID ABO59540 standard; cDNA; 603 BP.
XX ABO59540;

XX 02-AUG-2002 (first entry)

XX Human colon cancer related nucleotide sequence SEQ ID NO:3235.

XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.

XX Homo sapiens.

XX WO200229086-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US030732.

XX 02-OCT-2000; 2000US-0237271P.

XX (FARB) BAYER CORP.

XX Burgess C, Aetle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiaglingam A, Lewis ME;

XX WPI; 2002-426115/45.

PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.

XX Claim 1; Fig 1; 796bp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridizes to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the

CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists

XX
SQ Sequence 603 BP; 159 A; 119 C; 110 G; 206 T; 0 U; 9 Other;

Query Match 25.4%; Score 31.2; DB 6; Length 603;
Best Local Similarity 70.9%; Pred. No. 0.84;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGCTCTTAAGACCTGAAGAAACGCTAATAAGCCAAA 55
Db 567 GTTTCGGTGGCCCGGCTTTTAAANGNCCTTAAAGAAACGNTTAATAAAGCCAAA 513

RESULT 15
ABL69213/C
ID ABL69213 standard; DNA; 145831 BP.
XX ABL69213;

XX 15-MAY-2002 (first entry)

XX Prostate cancer related gene sequence SEQ ID NO:7550.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; wilm's tumour; adenocarcinoma;
KW gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.

PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0248678P.
PR 01-NOV-2000; 2000US-0245084P.

PA (AVAL-) AVALON PHARM.

PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;

DR WPI; 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 7550; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

SQ Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;

Query Match 25.2%; Score 31; DB 6; Length 145831;

Best Local Similarity 68.3%; Pred. No. 6.4;

Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 9300 CAGCTTACTTCAGACCTCCTCCAGGGTAGACAGATTGCACAGAACCACTCAATATTCTC 9241

QY 121 AAG 123

Db 9240 ATG 9238

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Job time : 163.422 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:16:28 ; Search time 35.927 Seconds
(without alignments)
2433.465 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	499	4 US-09-621-976-17307	Sequence 17307, A
2	123	100.0	2763	1 US-08-176-413-1	Sequence 1, Appli
3	123	100.0	2763	2 US-08-612-542B-1	Sequence 1, Appli
4	123	100.0	2763	2 US-08-772-113-1	Sequence 1, Appli
5	123	100.0	2763	3 US-09-199-137-1	Sequence 1, Appli
6	123	100.0	2763	4 US-08-227-800A-14	Sequence 14, Appl
7	123	100.0	2763	4 US-08-921-954-14	Sequence 14, Appl
8	123	100.0	2763	5 PCT-US94-14919-1	Sequence 1, Appli
9	123	100.0	2763	5 PCT-US94-14920-1	Sequence 1, Appli
10	123	100.0	3083	4 US-08-956-657-1	Sequence 25, Appl
11	123	100.0	3083	4 US-09-335-231-25	Sequence 25, Appl
12	123	100.0	796	4 US-09-270-767-5941	Sequence 5941, Ap
13	30.4	24.7	796	4 US-09-270-767-21223	Sequence 21223, A
14	28	22.8	2736	3 US-09-235-451-3	Sequence 3, Appli
15	28	22.8	2736	4 US-09-978-303-3	Sequence 3, Appli
16	27.2	22.1	1143	4 US-09-248-796A-5559	Sequence 5559, Ap
17	27	22.0	1025	4 US-09-270-767-4982	Sequence 4982, Ap
18	27	22.0	1025	4 US-09-270-767-20264	Sequence 20264, A
19	26.8	21.8	584	4 US-09-404-879A-268	Sequence 268, App
20	26.8	21.8	584	4 US-09-338-933-268	Sequence 268, App
21	26.8	21.8	584	4 US-09-215-681-268	Sequence 268, App
22	26.8	21.8	584	4 US-09-216-003A-268	Sequence 268, App
23	26.8	21.8	584	4 US-09-667-857-268	Sequence 268, App
24	26.6	21.6	1224	4 US-09-248-796A-5483	Sequence 5483, Ap
25	26.2	21.3	8106	3 US-09-135-241-1	Sequence 1, Appli
26	26	21.1	6669	4 US-10-204-708-6	Sequence 6, Appli
27	25.8	21.0	12847	1 US-08-550-715-1	Sequence 1, Appli

28	25.8	21.0	44453	3 US-09-146-053-5	Sequence 5, Appli
29	25.4	20.7	195	4 US-09-328-352-1949	Sequence 1949, Ap
30	25.4	20.7	699	4 US-09-583-110-1893	Sequence 1893, Ap
31	25.4	20.7	733	3 US-08-998-416-1027	Sequence 1027, Ap
32	25.4	20.7	1209	4 US-09-328-352-1076	Sequence 1076, Ap
33	25.4	20.7	5501	4 US-10-204-708-38	Sequence 38, Appl
34	25.4	20.7	10851	2 US-08-286-819A-16	Sequence 16, Appl
35	25.4	20.7	10851	3 US-08-980-357-16	Sequence 16, Appl
36	25.2	20.5	393	4 US-09-513-999C-23438	Sequence 23438, A
37	25.2	20.5	480	4 US-09-134-000C-1596	Sequence 1596, Ap
38	25.2	20.5	246240	2 US-08-724-394A-20	Sequence 20, Appl
39	25.2	20.5	246240	2 US-08-724-394A-21	Sequence 21, Appl
40	25.2	20.5	246240	2 US-08-724-394A-22	Sequence 22, Appl
41	25	20.3	443	4 US-09-513-999C-24786	Sequence 24786, A
42	25	20.3	1369	3 US-08-695-191-15	Sequence 15, Appl
43	25	20.3	1369	3 US-08-682-080-15	Sequence 15, Appl
44	25	20.3	1400	2 US-08-481-658B-43	Sequence 43, Appl
45	25	20.3	1400	2 US-08-477-504A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-17307
; Sequence 17307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Robert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17307
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-17307

Query Match 100.0%; Score 123; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTTAATAAGCCAAAGCTTA 60
DB 236 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTTAATAAGCCAAAGCTTA 295

QY 61 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGGTGAAGAAACCTTCATAACCTG 120
DB 296 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGGTGAAGAAACCTTCATAACCTG 355

QY 121 AAG 123
DB 356 AAG 358

RESULT 2
US-08-176-413-1
; Sequence 1, Application US/08176413
; Patent No. 5571510
; GENERAL INFORMATION:
; APPLICANT: NO. 5571510ori, Teutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,413
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: PD2864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-176-413-1

Query Match          100.0%; Score 123; DB 1; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAAGAAACGCTAATAAAGCCAAAGCTTA 60
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QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCCTCCATAACCTG 120
Db      1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCCTCCATAACCTG 1759

QY      121 AAG 123
Db      1760 AAG 1762

RESULT 3
US-08-612-542B-1
; Sequence 1, Application US/08612542B
; Patent No. 5840505
; GENERAL INFORMATION:
; APPLICANT: Carrera, Carlos J.
; APPLICANT: Cottam, Howard B.
; APPLICANT: No. 5840505or1, Tsutomu
; APPLICANT: Carson, Dennis A.
; TITLE OF INVENTION: METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
; TITLE OF INVENTION: ACTIVITY IN MALIGNANT METHYLTTHIOADENOSINE PHOSPHORYLASE DEFICI
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,542B
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: methyladenosine phosphatase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-612-542B-1

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Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCCTCCATAACCTG 1759

QY      121 AAG 123
Db      1760 AAG 1762

RESULT 4
US-08-772-113-1
; Sequence 1, Application US/08772113
; Patent No. 5942393
; GENERAL INFORMATION:
; APPLICANT: No. 5942393or1, Tsutomu
; APPLICANT: Carson, Dennis A.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: METHOD FOR DETECTION OF
; TITLE OF INVENTION: METHYLTTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,113
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/176,855
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-08-772-113-1

Query Match
Best Local Similarity 100.0%; Score 123; DB 2; Length 2763;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1640 GTTTCGGTGACCGGGTCTTAAGACCCCTGAAGAAACGCTAATAAGCCAAAGCTTA 1699

OY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759

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RESULT 5
US-09-199-137-1
Sequence 1, Application US/09199137
Patent No. 6214571
GENERAL INFORMATION:
APPLICANT: NO. 6214571ori, Tsutomu
APPLICANT: Carson, Dennis A.
APPLICANT: Carrera, Carlos J.
APPLICANT: Cottam, Howard B.
TITLE OF INVENTION: METHOD FOR DETECTION OF
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,137
FILING DATE: 24-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:

NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-09-199-137-1

Query Match
Best Local Similarity 100.0%; Score 123; DB 3; Length 2763;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTTCGGTGACCGGGTCTTAAGACCCCTGAAGAAACGCTAATAAGCCAAAGCTTA 60
|||
DB 1640 GTTTCGGTGACCGGGTCTTAAGACCCCTGAAGAAACGCTAATAAGCCAAAGCTTA 1699

OY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||
DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 1759

OY 121 AAG 123
|||
DB 1760 AAG 1762

RESULT 6
US-08-227-800A-14
Sequence 14, Application US/08227800A
Patent No. 6689561
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: NOBORI, TSUTOMU
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
TITLE OF INVENTION: DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANCER
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800A
FILING DATE: 14-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: Methylthioadenosine Phosphorylase (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2763
; US-08-227-800A-14

Query Match      100.0%; Score 123; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 60
Db      1640 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 1699

QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 120
Db      1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 1759

QY      121 AAG 123
Db      1760 AAG 1762

RESULT 7
US-08-921-954-14
; Sequence 14, Application US/08921954
; Patent No. 6689864
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; No. 6689864ori, Tautomu
; TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
; Detection of Cancer, Monitoring of Tumor Progression and
; Cancer Treatment
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,954
; FILING DATE: 26-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,671A
; FILING DATE: 18-Jul-2001
; APPLICATION NUMBER: US 08/921,954
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hirsch, Matthew E.
; REGISTRATION NUMBER: 47,651
; REFERENCE/DOCKET NUMBER: 023070-104042US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2763
; OTHER INFORMATION: /note="full-length
; methylthioadenosine phosphorylase
; (MTase) genomic nucleotide sequence"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 254..421
; FEATURE:
; NAME/KEY: exon
; LOCATION: 616..720
; FEATURE:
; NAME/KEY: exon
; LOCATION: 964..1203
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

Query Match      100.0%; Score 123; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 60
Db      1640 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAACGCTAATAAAGCCAAAGCTTA 1699

QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 120
Db      1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAAACCTCCATAACCTG 1759

QY      121 AAG 123
Db      1760 AAG 1762

RESULT 8
PCT-US94-14919-1
; Sequence 1, Application PC/TUS9414919
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
; TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14919
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-286
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14919-1

Query Match 100.0%; Score 123; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 60
DB 1640 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 1699
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCATAACCTG 120
DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCATAACCTG 1759
QY 121 AAG 123
DB 1760 AAG 1762

RESULT 9

PCT-US94-14920-1

Sequence 1, Application PC/TUS9414920

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY

APPLICANT: OF CALIFORNIA

TITLE OF INVENTION: METHOD FOR DETECTION OF

TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN

NUMBER OF INVENTIONS: CELLS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 N. Figueroa Street, 5th floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14920

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berliner, Robert

REGISTRATION NUMBER: 20,121

REFERENCE/DOCKET NUMBER: 5555-287

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-977-1001

TELEFAX: 213-977-1003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2763 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: methyladenosine phosphatase

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2763

PCT-US94-14920-1

Query Match 100.0%; Score 123; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 60
DB 1640 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 1699
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCATAACCTG 120
DB 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCCCTCATAACCTG 1759
QY 121 AAG 123
DB 1760 AAG 1762

RESULT 10

US-08-956-657-1

Sequence 1, Application US/08956657

Patent No. 6210917

GENERAL INFORMATION:

APPLICANT: No. 6210917ori et al., Tsutomu

TITLE OF INVENTION: METHOD FOR DETECTION OF

TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMALIAN

NUMBER OF INVENTIONS: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,657

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/827,342

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,855

FILING DATE: 29-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/050001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3083 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-956-657-1

Query Match 100.0%; Score 123; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 60
DB 2426 GTTTCGGTGAACCGGCTCTTAAGACCCCTGAAGAAACCGCTAATAAGCCAAAGCTTA 2485

QY 61 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATAACCTG 120
|||
Db 2486 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATAACCTG 2545
QY 121 AAG 123
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Db 2546 AAG 2548

RESULT 11
US-09-335-231-25
; Sequence 25, Application US/09335231
; Patent No. 6576420
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; TITLE OF INVENTION: Prognosis in, Cancer
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/09/335,231
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/090,411
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTAP) gene
; NAME/KEY: modified base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
US-09-335-231-25

Query Match 100.0%; Score 123; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.3e-34;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTTTAAAGACCTGAAGAAAGAAACGCTAATAAGCCAAAAGCTTA 60
|||
Db 2426 GTTTCGGTGAACCGGCTTTAAAGACCTGAAGAAAGAAACGCTAATAAGCCAAAAGCTTA 2485
QY 61 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATAACCTG 120
|||

Db 2486 CTGCTACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCTCCATAACCTG 2545
QY 121 AAG 123
|||
Db 2546 AAG 2548

RESULT 12
US-09-270-767-5941/C
; Sequence 5941, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5941
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5941

Query Match 24.7%; Score 30.4; DB 4; Length 796;
Best Local Similarity 57.3%; Pred. No. 0.22;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 19 TTAAGACCCCTGAAGAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTACCATACCT 78
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Db 193 TTGCAACACACATAAAATATATATAAATTAAAGCAAAAGCTTACTCACCAGAACGATACCT 134
QY 79 CAGATAGGGTCCACAGAAATGTCAGAAACCTTCAT 114
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Db 133 GTACTAATTTTACGAAATCTTTCGAAACACTTCAT 98

RESULT 13
US-09-270-767-21223/C
; Sequence 21223, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21223
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-21223

Query Match 24.7%; Score 30.4; DB 4; Length 796;
Best Local Similarity 57.3%; Pred. No. 0.22;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 19 TTAAGACCCCTGAAGAAACGCTAATAAAGCCAAAAGCTTACTGCTCACTACCATACCT 78
|||
Db 193 TTGCAACACACATAAAATATATATAAATTAAAGCAAAAGCTTACTCACCAGAACGATACCT 134
QY 79 CAGATAGGGTCCACAGAAATGTCAGAAACCTTCAT 114
|||
Db 133 GTACTAATTTTACGAAATCTTTCGAAACACTTCAT 98

RESULT 14
US-09-235-451-3
; Sequence 3, Application US/09235451
; GENERAL INFORMATION:

APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 9076/084CIP
CURRENT APPLICATION NUMBER: US/09/235,451
CURRENT FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 3
LENGTH: 2736
TYPE: DNA
ORGANISM: R. rattus
FEATURE:
US-09-235-451-3

Query Match 22.8%; Score 28; DB 3; Length 2736;
Best Local Similarity 55.0%; Pred. No. 2.5;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 11 ACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAGCTTACTGCTCACTA 70
DB 1207 ACCAAGGCTTCACACCCCTGAAGCTAGCCGCAAGGAAGCAAAATCGAGATTTTCAGGC 1266
OY 71 CCATACCTCAGATAGGGTCCACAGAAATGCTCAGAAACCT 110
DB 1267 ACATCTGCAGCGGGAATTCTCAGAGACCGTACCAGCCCT 1306

RESULT 15
US-09-978-303-3
Sequence 3, Application us/09978303
Patent No. 6790629
GENERAL INFORMATION:
APPLICANT: Julius, David J.
APPLICANT: Caterina, Michael J.
APPLICANT: Brake, Anthony J.
TITLE OF INVENTION: Nucleic acid sequences encoding
TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
TITLE OF INVENTION: polypeptides and uses thereof
FILE REFERENCE: UCAL084CON
CURRENT APPLICATION NUMBER: US/09/978,303
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/235,451
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/072,151
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 08/915,461
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 3
LENGTH: 2736
TYPE: DNA
ORGANISM: R. rattus
US-09-978-303-3

Query Match 22.8%; Score 28; DB 4; Length 2736;
Best Local Similarity 55.0%; Pred. No. 2.5;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 11 ACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAGCTTACTGCTCACTA 70
DB 1207 ACCAAGGCTTCACACCCCTGAAGCTAGCCGCAAGGAAGCAAAATCGAGATTTTCAGGC 1266
OY 71 CCATACCTCAGATAGGGTCCACAGAAATGCTCAGAAACCT 110

DB 1267 ACATCTGCAGCGGGAATTCTCAGAGACCGTACCAGCCCT 1306

Search completed: February 1, 2005, 15:01:05
Job time : 36.927 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 169.156 Seconds
(without alignments)
4178.057 Million cell updates/sec

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Sequence: 1 GTTTCGGTGACCGGCTCTT.....AAACCTCATTAACCTGAAG 123

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8600550

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	123	100.0	2269	US-10-779-476-2	Sequence 2, Appli
3	123	100.0	2763	US-09-908-671-14	Sequence 14, Appli
4	123	100.0	3083	US-09-780-114-1	Sequence 1, Appli
5	123	100.0	3083	US-10-326-681-25	Sequence 25, Appli
6	113	91.9	1437	US-10-106-698-749	Sequence 749, App
7	41.2	33.5	662	US-09-969-034-2820	Sequence 2820, Ap
8	31.8	25.9	3186778	US-10-027-632-174961	Sequence 174961,
9	31.8	25.9	3186778	US-10-027-632-174961	Sequence 174961,
10	31.2	25.4	603	US-09-969-034-3235	Sequence 3235, Ap
11	31	25.2	145831	US-09-969-708-79	Sequence 79, Appli
12	31	25.2	145831	US-09-954-456-2116	Sequence 2116, Ap

C 13	31	25.2	145831	10	US-09-873-367C-646	Sequence 646, App
C 14	31	25.2	145831	11	US-09-968-007A-455	Sequence 455, App
C 15	31	25.2	145831	16	US-10-240-425-363	Sequence 363, App
C 16	29.8	24.2	760	18	US-10-363-345A-3575	Sequence 3575, Ap
C 17	29.8	24.2	760	18	US-10-363-345A-3576	Sequence 3576, Ap
C 18	29.2	23.7	2207	15	US-10-331-496A-84	Sequence 84, Appli
C 19	29.2	23.7	2940917	13	US-10-027-632-174763	Sequence 174763,
C 20	29.2	23.7	2940917	15	US-10-027-632-174763	Sequence 174763,
C 21	29	23.6	7746	15	US-10-311-455-1829	Sequence 1829, Ap
C 22	29	23.6	7746	16	US-10-257-166-129	Sequence 129, App
C 23	28.8	23.4	2891	15	US-10-080-381B-72	Sequence 72, Appli
C 24	28.8	23.4	211257	13	US-10-087-192-529	Sequence 529, App
C 25	28.6	23.3	237	18	US-10-425-115-174545	Sequence 174545,
C 26	28.6	23.3	339	18	US-10-425-115-148116	Sequence 148116,
C 27	28.4	23.1	499	13	US-10-027-632-310136	Sequence 310136,
C 28	28.4	23.1	499	15	US-10-027-632-310136	Sequence 310136,
C 29	28.4	23.1	14112	15	US-10-311-455-1415	Sequence 1415, Ap
C 30	28.4	23.1	14112	16	US-10-221-714A-199	Sequence 199, App
C 31	28.4	23.1	14112	17	US-10-433-793-9	Sequence 9, Appli
C 32	28.4	23.1	392112	18	US-10-812-232-3	Sequence 3, Appli
C 33	28.2	22.9	609	13	US-10-027-632-197273	Sequence 197273,
C 34	28.2	22.9	609	15	US-10-027-632-197273	Sequence 197273,
C 35	28.2	22.9	688	13	US-10-027-632-201264	Sequence 201264,
C 36	28.2	22.9	688	13	US-10-027-632-201265	Sequence 201265,
C 37	28.2	22.9	688	13	US-10-027-632-201266	Sequence 201266,
C 38	28.2	22.9	688	13	US-10-027-632-201267	Sequence 201267,
C 39	28.2	22.9	688	13	US-10-027-632-201268	Sequence 201268,
C 40	28.2	22.9	688	15	US-10-027-632-201264	Sequence 201264,
C 41	28.2	22.9	688	15	US-10-027-632-201265	Sequence 201265,
C 42	28.2	22.9	688	15	US-10-027-632-201265	Sequence 201265,
C 43	28.2	22.9	688	15	US-10-027-632-201266	Sequence 201266,
C 44	28.2	22.9	688	15	US-10-027-632-201267	Sequence 201267,
C 45	28.2	22.9	688	15	US-10-027-632-201268	Sequence 201268,

ALIGNMENTS

RESULT 1
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Pei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skaltitzky, Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; TITLE OF INVENTION: Phosphorylase Deficient Cells
; FILE REFERENCE: PC19080A (AG10-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned M7AP cDNA
US-10-367-366-1

Query Match 100.0%; Score 123; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTTCGGTGACCGGCTCTTAAGACCTGAAGAAAGCGTAATTAAGCCAAAGCTTA 60
|||||

Db 697 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAAGAAAAACGCTAATAAAGCCAAAGCTTA 756
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 120
Db 757 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 816
QY 121 AAG 123
Db 817 AAG 819

RESULT 2
US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
; APPLICANT: Salmelix, Inc.
; APPLICANT: Leonl, Lorenzo M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
; FILE REFERENCE: 076936-0307942
; CURRENT APPLICATION NUMBER: US/10/779,476
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,888
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/460,715
; PRIOR FILING DATE: 2004-04-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-476-2

Query Match 100.0%; Score 123; DB 18; Length 2269;
Best Local Similarity 100.0%; Pred. No. 2.4e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
Db 812 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAAGAAAAACGCTAATAAAGCCAAAGCTTA 871
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 120
Db 872 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 931
QY 121 AAG 123
Db 932 AAG 934

RESULT 3
US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; NOBORI, TSUTOMU
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
; DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
; TREATMENT
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthioadenosine Phosphorylase (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

Query Match 100.0%; Score 123; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.5e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
Db 1640 GTTTCGGTGGACCGGCTTTAAAGACCCCTGAAAGAAAAACGCTAATAAAGCCAAAGCTTA 1699
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 120
Db 1700 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 1759
QY 121 AAG 123
Db 1760 AAG 1762

RESULT 4
US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020146695A1ori, Tsutomu
; Carson, Dennis A.
; Takabayashi, Kenji
; TITLE OF INVENTION: Method for Detection of the Presence or
; Absence of Methylthioadenosine Phosphorylase
; (MTase) in a
; Cell Sample by Detection of the Presence or Absence
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/780,114
FILING DATE: 09-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,914
FILING DATE: 04-May-1998
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/459,343
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/827,342
FILING DATE: 26-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-103030US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..3083
OTHER INFORMATION: /note= "rat methylchloadenosine
phosphorylase (MTase)"
FEATURE:
NAME/KEY: exon
LOCATION: 119..151
OTHER INFORMATION: /note= "exon 1"
FEATURE:
NAME/KEY: exon
LOCATION: 450..536
OTHER INFORMATION: /note= "exon 2"
FEATURE:
NAME/KEY: exon
LOCATION: 724..782
OTHER INFORMATION: /note= "exon 3"
FEATURE:
NAME/KEY: exon
LOCATION: 899..1066
OTHER INFORMATION: /note= "exon 4"
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1480
OTHER INFORMATION: /note= "exon 5"
FEATURE:
NAME/KEY: exon
LOCATION: 1764..1953
OTHER INFORMATION: /note= "exon 6"
FEATURE:
NAME/KEY: exon
LOCATION: 2426..2548
OTHER INFORMATION: /note= "exon 7"
FEATURE:
NAME/KEY: exon
LOCATION: 2838..2876
OTHER INFORMATION: /note= "exon 8"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

Query Match 100.0%; Score 123; DB 9; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.6e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTTCGTGACCGGGTCTTAAGACCTGAAGAAAGCGCTAATAAGCCAAAGCTTA 60
|||||

Db 2426 GTTTCGTGACCGGGTCTTAAGACCTGAAGAAAGCGCTAATAAGCCAAAGCTTA 2485
QY 61 CTGCTCACTACCATACCTAGATAGGGTCCACAGATGCTCAGAAACCTCCATACCTG 120
Db 2486 CTGCTCACTACCATACCTAGATAGGGTCCACAGATGCTCAGAAACCTCCATACCTG 2545
QY 121 AAG 123
Db 2546 AAG 2548

RESULT 5
US-10-326-681-25
Sequence 25, Application US/10326681
Publication No. US20030175768A1
GENERAL INFORMATION:
APPLICANT: Carson, Dennis A.
APPLICANT: Schmid, Mathias
APPLICANT: Carrera, Carlos J.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
FILE REFERENCE: 023070-108010US
CURRENT APPLICATION NUMBER: US/10/326,681
PRIOR FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US 60/090,411
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 3083
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: genomic sequence for methylchloadenosine
phosphorylase (MTAP) gene
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(3083)
OTHER INFORMATION: n = unknown
FEATURE:
NAME/KEY: exon
LOCATION: (119)..(151)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (450)..(536)
OTHER INFORMATION: exon 2
FEATURE:
NAME/KEY: exon
LOCATION: (724)..(782)
OTHER INFORMATION: exon 3
FEATURE:
NAME/KEY: exon
LOCATION: (899)..(1066)
OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: (1378)..(1480)
OTHER INFORMATION: exon 5
FEATURE:
NAME/KEY: exon
LOCATION: (1764)..(1953)
OTHER INFORMATION: exon 6
FEATURE:
NAME/KEY: exon
LOCATION: (2426)..(2548)
OTHER INFORMATION: exon 7
FEATURE:
NAME/KEY: exon
LOCATION: (2838)..(2876)
OTHER INFORMATION: exon 8
US-10-326-681-25

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Query Match          100.0%; Score 123; DB 15; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.6e-31;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGGACCGGGTCTTAAGACCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 60
      |||
Db      2426 GTTTCGGTGGACCGGGTCTTAAGACCTGAAAGAAAACGCTAATAAGCCAAAAGCTTA 2485

QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCTCCATAACCTG 120
      |||
Db      2486 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCTCCATAACCTG 2545

QY      121 AAG 123
      |||
Db      2546 AAG 2548
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```
RESULT 6
US-10-106-698-749
; Sequence 749, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 749
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-749
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```
Query Match          91.9%; Score 113; DB 15; Length 1437;
Best Local Similarity 95.0%; Pred. No. 5.2e-28;
Matches 113; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      5 CGGTGACCGGGTCTTAAGACCTGAAAGAAAACGCTAATAAGCCAAAAGCTTACTGC 64
      |||
Db      1 CGGTGACCGGTCTTAAGACCTGAAAGAAAACGCTAATAAGCCAAAAGCTTACTGC 60

QY      65 TCACCTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCTCCATAACCTGAAG 123
      |||
Db      61 TCACCTACCATACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCTCCATAACCTGAAG 119
```

```
RESULT 7
US-09-969-034-2820
; Sequence 2820, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Ascle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
```

```
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2820
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 51, 127, 216, 234, 235, 240, 289, 315, 338, 362, 365, 390,
; LOCATION: 402, 405, 410, 411, 432, 436, 442, 460, 466, 487, 493, 506,
; LOCATION: 509, 512, 525, 526, 537, 551, 560, 566, 570, 576, 581, 583,
; LOCATION: 588, 609, 611, 621, 632, 636, 649, 657
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-2820
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Query Match          33.5%; Score 41.2; DB 11; Length 662;
Best Local Similarity 71.3%; Pred. No. 0.00099;
Matches 87; Conservative 0; Mismatches 30; Indels 5; Gaps 3;
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QY      2 TTTGGGTGACCGGGTCTTAAGACCCCTGAAG--AAAACGCTAATAAGCCA-AAAGCT 58
      |||
Db      444 TTCCGGTGACCGGGTCTTAAGACCCCTGAAGGAAAACCGCTNTTAANCCATTAAGCT 503

QY      59 TACTGCTCACTACCA--TACCTCAGATAGGGTCCACAGAAATGTCAGAAACCCTCATTA 116
      |||
Db      504 TANTGNTCNATTACCAATACCTNAGATAGGGTCNCAAAATGTCANAAAAACCTCNATA 563

QY      117 CC 118
      ||
Db      564 CC 565
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```
RESULT 8
US-10-027-632-174961
; Sequence 174961, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174961
; LENGTH: 3186778
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
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```
Query Match          25.9%; Score 31.8; DB 13; Length 3186778;
Best Local Similarity 58.1%; Pred. No. 21;
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Matches 54; Conservative 1; Mismatches 38; Indels 0; Gaps 0;

QY 3 TTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGTAATTAAGCCAAAGCTTACT 62

Db 1986449 TTCGATAGTCCGGTATTGGTACTAAKTGATTAAACTCCATGAAATCCAAAGCCCATATA 1986508

QY 63 GCTCACTACCATACCTCAGATAGGGTCCACAGA 95

Db 1986509 GATCAACAATAAGTCCACCAGGGTCGGAGA 1986541

RESULT 9

US-10-027-632-174961

; Sequence 174961, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 174961

; LENGTH: 3186778

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(3186778)

; OTHER INFORMATION: n = A,T,C or G

US-10-027-632-174961

Query Match 25.9%; Score 31.8; DB 15; Length 3186778;

Best Local Similarity 58.1%; Pred. No. 21;

Matches 54; Conservative 1; Mismatches 38; Indels 0; Gaps 0;

QY 3 TTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGTAATTAAGCCAAAGCTTACT 62

Db 1986449 TTCGATAGTCCGGTATTGGTACTAAKTGATTAAACTCCATGAAATCCAAAGCCCATATA 1986508

QY 63 GCTCACTACCATACCTCAGATAGGGTCCACAGA 95

Db 1986509 GATCAACAATAAGTCCACCAGGGTCGGAGA 1986541

RESULT 10

US-09-969-034-3235/C

; Sequence 3235, Application US/09969034

; Publication No. US20040110668A1

; GENERAL INFORMATION:

; APPLICANT: Burgess, Christopher C.

; APPLICANT: Aetle, Jon H.

; APPLICANT: Carroll, Eddie III

; APPLICANT: Catino, Theodore J.

; APPLICANT: Dwivedi, Poorima

; APPLICANT: Molino, Gary A.

; APPLICANT: Thiagalingam, Arunthathi

; APPLICANT: Lewis, Marcia E.

; TITLE OF INVENTION: Nucleic Acid Sequences Differentially

; TITLE OF INVENTION: Expressed in Cancer Tissue

; FILE REFERENCE: 1657/1032

; CURRENT APPLICATION NUMBER: US/09/969,034

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/237,271

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 4494

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3235

; LENGTH: 603

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 492, 497, 506, 527, 542, 544, 573, 576, 597

; OTHER INFORMATION: n = A,T,C or G

US-09-969-034-3235

Query Match 25.4%; Score 31.2; DB 11; Length 603;

Best Local Similarity 70.9%; Pred. No. 2.4;

Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 GTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGTAATTAAGCCAAAA 55

Db 567 GTTCGGTGCCCGGGTTTAAAGNCCCTTAAAGAAAGCGTTAATAAGCCAAA 513

RESULT 11

US-09-969-708-79/C

; Sequence 79, Application US/09969708

; Patent No. US20020102532A1

; GENERAL INFORMATION:

; APPLICANT: Augustus, Meena

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-70

; CURRENT APPLICATION NUMBER: US/09/969,708

; CURRENT FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: US/60/237,606

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: US/60/237,608

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: US/60/237,425

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 658

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 145831

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-969-708-79

Query Match 25.2%; Score 31; DB 9; Length 145831;

Best Local Similarity 68.3%; Pred. No. 15;

Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGCTGAGAAACCTCCATACCTG 120

Db 9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAAGCACTCAATATTCTC 9241

QY 121 AAG 123

Db 9240 ATG 9238

RESULT 12

US-09-954-456-2116/C

; Sequence 2116, Application US/09954456

; Patent No. US20020115057A1

; GENERAL INFORMATION:

; APPLICANT: Young, Paul

```
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2116
; LENGTH: 145831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2116
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Db      9300 CAGCTTACTTCAGACCTCCTCCAGGGTAGACAGATTGCACAGAACCACTCAATATTCTC 9241
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QY      121 AAG 123
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Db      9240 ATG 9238
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RESULT 13
US-09-873-367C-646/c
; Sequence 646, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 646
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; LENGTH: 145831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-646
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Best Local Similarity 68.3%; Pred. No. 15;
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QY      121 AAG 123
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Db      9240 ATG 9238
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RESULT 14
US-09-968-007A-455/c
; Sequence 455, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 455
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-455
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Best Local Similarity 68.3%; Pred. No. 15;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db      9300 CAGCTTACTTCAGACCTCCTCCAGGGTAGACAGATTGCACAGAAACCACTCAATATTCTC 9241
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QY      121 AAG 123
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Db      9240 ATG 9238
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RESULT 15
US-10-240-425-363/c
; Sequence 363, Application US/10240425
; Publication No. US20040033502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
```

APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 363
LENGTH: 145831
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF001548
US-10-240-425-363

Query Match 25.2%; Score 31; DB 16; Length 145831;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGCTCAGAAACCTCCATAACCTG 120
Db 9300 CAGCTTACTTCCAGACCTCCTCCAGGGTAGACAGATTGCACAGAGCACTCAATATTCTC 9241
QY 121 AAG 123
Db 9240 ATG 9238

Search completed: February 1, 2005, 17:20:44
Job time : 181.156 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 1382.94 Seconds
(without alignment)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_2426_2548
Perfect score: 123
Sequence: 1 GTTTCGGTGACCGGGTCTT.....AAACCTTCATTAAGCTGAAG 123

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	123	100.0	570	6	CD364939	CD364939 UI-H-FT2-
2	123	100.0	612	7	CN409515	CN409515 170006001
3	123	100.0	638	7	CN409513	CN409513 170005327
4	123	100.0	681	4	BM784030	BM784030 K-EST0062
5	123	100.0	684	6	CD364946	CD364946 UI-H-FT2-
6	123	100.0	774	2	BE538925	BE538925 601061292
7	123	100.0	813	9	AY405891	AY405891 Homo sapi
8	123	100.0	836	1	AL048242	AL048242 DKFZp5860
9	123	100.0	975	4	BM472910	BM472910 AGENCOURT
10	123	100.0	1064	5	BX459089	BX459089 BX459089
11	123	100.0	1380	3	BC012316	BC012316 Homo sapi
12	123	100.0	3028	3	BSM808193	BSM808193 Homo sapi
13	121.4	98.7	205	2	BF431095	BF431095 7007b11.x
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16	119.4	97.1	580	4	BM839857	BM839857 K-EST0116
17	119.4	97.1	580	4	BM840883	BM840883 K-EST0118
18	118.8	96.6	903	5	BX371508	BX371508 BX371508
19	118	95.9	330	5	BX102948	BX102948 BX102948
20	118	95.9	562	7	CN409511	CN409511 170006000
21	116.6	94.8	911	5	BX350035	BX350035 BX350035
22	113.4	92.2	1047	4	BM925551	BM925551 AGENCOURT
23	112.4	91.4	813	9	AY405892	AY405892 Pan trogl
24	112	91.1	491	1	AA635142	AA635142 afl10e10.s

25	111	90.2	819	2	BF981023	BF981023 602310222
26	110.4	89.8	1075	1	AL543068	AL543068 AL543068
27	110.2	89.6	429	1	AV667881	AV667881 AV667881
28	110.2	89.6	477	4	BG938257	BG938257 1AB014E09
29	110.2	89.6	484	7	CF930825	CF930825 CF--05-R-
30	110.2	89.6	562	4	BI774611	BI774611 466793 MA
31	110.2	89.6	581	6	CB538214	CB538214 776179 MA
32	110.2	89.6	586	7	CN441464	CN441464 BE04026A1
33	110.2	89.6	600	7	CO701132	CO701132 DG32-195b
34	110.2	89.6	682	7	CN788377	CN788377 4122709 B
35	110.2	89.6	950	7	CF413058	CF413058 CH3#083 G
36	107.6	87.5	568	7	CO586973	CO586973 DG2-139T1
37	106.6	86.7	692	7	CK968775	CK968775 4084058 B
38	105.4	85.7	421	1	AJ667166	AJ667166 AJ667166
39	103	83.7	401	1	AI674711	AI674711 wd19e10.x
40	100.6	81.8	679	2	AW150875	AW150875 xg41d10.x
41	99	80.5	885	5	BX374675	BX374675 BX374675
42	95.8	77.9	303	6	CA535795	CA535795 C0224B10-
43	95.8	77.9	443	6	CA536077	CA536077 C0228H03-
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ALIGNMENTS

RESULT 1
CD364939/c 570 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION UI-H-FT2-bjn-i-17-0-UI.81 NCI_CGAP_FT2 Homo sapiens CDNA clone
UI-H-FT2-bjn-i-17-0-UI 3', mRNA sequence.

ACCESSION CD364939
VERSION CD364939.1 GI:31149029
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 570)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html

Seq primer: M13 FORWARD
POLYA=Yes.
location/Qualifiers

1. 570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="UI-H-FT2-bjn-i-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;

NCI_CGAP_FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of

the conditions). The mRNA samples were pooled for library
conditions).

construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 123; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 7.4e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAAGACCTGAAGAAAACGCTAATAAGCCAAAGCTTA 60
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Db 527 GTTTCGGTGACCGGGTCTTAAAGACCTGAAGAAAACGCTAATAAGCCAAAGCTTA 468

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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Db 467 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 408

QY 121 AAG 123
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Db 407 AAG 405

RESULT 2
CN409515 612 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600188932 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION
ACCESSION CN409515
VERSION CN409515.1 GI:47396639
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 612)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 612 Std Error: 0.00.

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_lib="GRN_PREHEP"
/note="oligo dT primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAAGACCTGAAGAAAACGCTAATAAGCCAAAGCTTA 60
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Db 107 GTTTCGGTGACCGGGTCTTAAAGACCTGAAGAAAACGCTAATAAGCCAAAGCTTA 166

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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Db 167 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 226

QY 121 AAG 123
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Db 227 AAG 229

RESULT 3

CN409513 638 bp mRNA linear EST 16-MAY-2004
LOCUS 17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION
ACCESSION CN409513
VERSION CN409513.1 GI:47396637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 638)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 638 Std Error: 0.00.

FEATURES
source location/Qualifiers
1. .638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Query Match 100.0%; Score 123; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 468 GTTTCGGTGACCGGGTCTTAAAGACCTGAAGAAAACGCTAATAAGCCAAAGCTTA 527

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
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Db 528 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 587

QY 121 AAG 123
|||

Db	588	AA	G	590
RESULT 4				
BM784030				
LOCUS				
DEFINITION	BM784030	681 bp	mRNA	linear EST 05-MAR-2002
	K-EST0062086 S6SNU620 Homo sapiens	CDNA clone S6SNU620-32-F01 5',		
	mRNA sequence.			
ACCESSION	BM784030			
VERSION	BM784030.1	GI:19132262		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	1 (bases 1 to 681)			
REFERENCE	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,			
AUTHORS	Oh,K.Y., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and			
	Kim,Y.S.			
	21C Frontier Korean EST Project 2001			
	Unpublished (2002)			
TITLE	Contact: Kim YS			
JOURNAL	Genome Research Center			
COMMENT	Korea Research Institute of Bioscience & Biotechnology			
	52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea			
	Tel: +82-42-860-4470			
	Fax: +82-42-860-4409			
	Email: yongsung@mail.kribb.re.kr			
	Plate: 32 row: F column: 01			
	High quality sequence stop: 681.			

FEATURES	Location/Qualifiers
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1. .681
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/sex="F"
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/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/clone_11b="S6SNU620"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including Ecor
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

```

ORIGIN

Query Match	100.0%;	Score 123;	DB 4;	Length 681;
Best Local Similarity	100.0%;	Pred. No. 7.6e-29;		
Matches 123; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy 1 GTTTCGGTGACCCGGGTCTTTAAAGACCCTGAAGAAGAACGCTAATTAAGCCAAAAGCTTA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 189 GTTTCGGTGACCCGGGTCTTTAAAGACCCTGAAGAAGAACGCTAATTAAGCCAAAAGCTTA 248

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Oy      61 CTGCTCACTACCATACCCTCAGATAGGGTCCACGAATGGTCAGAAACCTTCATAA CCGT   120
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QY 121 AAG 123

Db 309 AAG 311

RESULT 5	684 bp	mRNA	linear	EST 05-AUG-2004
CD364946/c				
LOCUS				
DEFINITION				
UI-H-FT2-bjn-k-07-0-UI	s1	NCI CGAP	FT2 Homo sapiens	CDNA clone
UI-H-FT2-bjn-k-07-0-UI	3'	mRNA sequence.		

ACCESSION	CD364946
VERSION	CD364946.1
KEYWORDS	GI:31149036 EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 684)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cdNA Library preparation: Dr. M. Bento Soares, University of Iowa
cdNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at:

<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD

FEATURES

Location/Qualifiers

Source

1..684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-k-07-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_FT2 is a substracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GCCCCATGCCG"

ORIGIN

Query Match	100.0%;	Score 123;	DB 6;	Length 684;
Best Local Similarity	100.0%;	Pred. No. 7.6e-29;		
Matches 123; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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QY      1 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
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Db      527 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 468
QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 120
      |||
Db      467 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 408
QY      121 AAG 123
      |||
Db      407 AAG 405

RESULT 6
LOCUS   BE538925
DEFINITION 601061292F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447622 5',
      mRNA sequence.
ACCESSION BE538925 774 bp mRNA linear EST 09-AUG-2000
VERSION BE538925
KEYWORDS BE538925.1 GI:9767570
SOURCE EST.
ORGANISM Homo sapiens (human)
      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 774)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
      National Institutes of Health, Mammalian Gene Collection (MGC)
      Unpublished (1999)
      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-r@mail.nih.gov
      Tissue Procurement: ATCC
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: Incyte Genomics, Inc.
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.lnl.gov
      Plate: LHAM8421 row: h column: 23
      High quality sequence stop: 615.
      Location/Qualifiers
        1..774
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:3447622"
        /cell_line="MGC36"
        /lab_host="DH10B"
        /clone_lib="NIH MGC 10"
        /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
        Average insert size 1.5 kb. Library prepared by Life
        Technologies."

ORIGIN

Query Match 100.0%; Score 123; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 7.8e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
      |||
Db      127 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 186
QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 120
      |||
Db      187 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAATGCTCAGAAACCCCTCCATAACCTG 246
QY      121 AAG 123
      |||
Db      247 AAG 249
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```
RESULT 7
LOCUS   AY405891
DEFINITION Homo sapiens MTAP gene, VIRTUAL TRANSCRIPT, partial sequence,
      genomic survey sequence.
ACCESSION AY405891
VERSION AY405891.1 GI:39761865
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 813)
REFERENCE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Inferring nonneutral evolution from human-chimp-mouse orthologous
      gene trios
      Science 302 (5652), 1960-1963 (2003)
      14671302
      2 (bases 1 to 813)
REFERENCE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Direct Submission
      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
      Rockville, MD 20850, USA
      This sequence was made by sequencing genomic exons and ordering
      them based on alignment.
      Location/Qualifiers
        1..813
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        <1..>813
        /gene="MTAP"
        /locus_tag="HCM2375"

ORIGIN

Query Match 100.0%; Score 123; DB 9; Length 813;
Best Local Similarity 100.0%; Pred. No. 7.9e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 60
      |||
Db      691 GTTTCGGTGAACCGGGTCTTAAAGACCTGAAGAAAAACGCTAATAAAGCCAAAGCTTA 750
QY      61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGCTCAGAAACCCCTCATTAACCTG 120
      |||
Db      751 CTGCTCACTACCATACCTCAGATAGGGTCCACAGAAATGCTCAGAAACCCCTCATTAACCTG 810
QY      121 AAG 123
      |||
Db      811 AAG 813

RESULT 8
LOCUS   AL048242
DEFINITION AL048242 836 bp mRNA linear EST 04-SEP-2003
      DKFZ586O1023_r1 586 (synonym: hute1) Homo sapiens cDNA clone
      DKFZ586O1023, mRNA sequence.
      AL048242
      AL048242.1 GI:4729075
      AL048242
      EST.
      Homo sapiens (human)
      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 836)
REFERENCE Ansoorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
      EST (Ansoorge, et al.)
```

JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@kitz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp586O1023) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source Location/Qualifiers
1. 836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp586O1023"
/tissue_type="uterus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="586 (synonym: hutel)"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI/MluI"

ORIGIN

Query Match 100.0%; Score 123; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 7.9e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 60
|||||
Db 198 GTTTCGGTGAACCGGCTTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 257
61 CTGCTCACTACCATATCCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||||
Db 258 CTGCTCACTACCATATCCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 317

QY 121 AAG 123
|||
Db 318 AAG 320

RESULT 9
BM472910 975 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6466233 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574548
DEFINITION 5', mRNA sequence.
ACCESSION BM472910
VERSION BM472910.1 GI:18521952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 975)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12323 row: f column: 21
High quality sequence stop: 636.
Location/Qualifiers
1. 975

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5574548"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC library."

ORIGIN

Query Match 100.0%; Score 123; DB 4; Length 975;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGAACCGGCTTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 60
|||||
Db 166 GTTTCGGTGAACCGGCTTTAAAGACCTGAAAGAAACGCTAATAAGCCAAAGCTTA 225
61 CTGCTCACTACCATATCCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 120
|||||
Db 226 CTGCTCACTACCATATCCTCAGATAGGGTCCACAGAATGTCAGAAACCTCCATAACCTG 285

QY 121 AAG 123
|||
Db 286 AAG 288

RESULT 10
BX459089 1064 bp mRNA linear EST 06-MAY-2004
LOCUS BX459089 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YH01
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX459089
VERSION BX459089.2 GI:47066799
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1064)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31029072.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cs=CS0DE012CD01QP1&c=5445.f>.

FEATURES
source Location/Qualifiers
1. 1064
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YH01"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 100.0%; Score 123; DB 5; Length 1064;
Best Local Similarity 100.0%; Pred. No. 8.3e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAGAGAAACGCTAATAAAGCCAAAGCTTA 60
|||||
Db 660 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAGAGAAACGCTAATAAAGCCAAAGCTTA 719

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGCTCAGAAAACCTCCATAACCTG 120
|||||
Db 720 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGCTCAGAAAACCTCCATAACCTG 779

QY 121 AAG 123
|||
Db 780 AAG 782

RESULT 11
BC012316 1380 bp mRNA linear HTC 19-NOV-2003
LOCUS Homo sapiens methylthioadenosine phosphorylase, mRNA (cDNA clone
IMAGE:3546198), containing frame-shift errors.
ACCESSION BC012316 GI:15147365
VERSION BC012316.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1380)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1380)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven
Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 8 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 6006025
This clone has the following problem: frame shifted.

FEATURES
source
1..1380
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3546198"
/tissue_type="Placenta, choriocarcinoma"
/clone_id="NIH MGC_21"
/lab_host="DH10B-R"
/note="Vector: POTB7"

ORIGIN

Query Match 100.0%; Score 123; DB 3; Length 1380;
Best Local Similarity 100.0%; Pred. No. 8.6e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAGAGAAACGCTAATAAAGCCAAAGCTTA 60
|||||
Db 795 GTTTCGGTGGACCGGGTCTTAAAGACCCCTGAAGAGAAACGCTAATAAAGCCAAAGCTTA 854

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGCTCAGAAAACCTCCATAACCTG 120
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Db 855 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGCTCAGAAAACCTCCATAACCTG 914

QY 121 AAG 123
|||
Db 915 AAG 917

RESULT 12
HSM808193/c 3028 bp mRNA linear HTC 03-AUG-2004
LOCUS HSM808193
DEFINITION Homo sapiens mRNA; cDNA DKFZp686O20193 (from clone DKFZp686O20193).
ACCESSION BX648047
VERSION BX648047.1 GI:34367206
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3028)
AUTHORS Ansoorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Well,B., Amd,C., Osanger,A., Fobo,G., Han,W. and
Wiemann,S.
The German cDNA Consortium
CONSRM Direct Submission
TITLE Submitted (13-JUL-2004) MIPS, Ingolstaedter Landstr.1, D-85764
JOURNAL Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686O20193) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686O20193>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.
Location/Qualifiers

FEATURES
Location/Qualifiers

Source 1. 3028
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686C20193"
/tissue_type="esophagus tumor"
/clone_lib="686 (synonym: hicc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="unclassified"

ORIGIN

Query Match 100.0%; Score 123; DB 3; Length 3028;
Best Local Similarity 100.0%; Pred. No. 9.9e-29;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGCTTTAAGACCCCTGAAAAAGAAACGCTAATAAGCCAAAGCTTA 60
|||
DB 2627 GTTTCGGTGACCGGGCTTTAAGACCCCTGAAAAAGAAACGCTAATAAGCCAAAGCTTA 2568

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTCAGAAACCTCCATTAACCTG 120
|||
DB 2567 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTCAGAAACCTCCATTAACCTG 2508

QY 121 AAG 123
|||
DB 2507 AAG 2505

RESULT 13
BF431095/c 205 bp mRNA linear EST 29-NOV-2000
LOCUS 7007b11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3573452 3'
DEFINITION similar to SW:MTAP HUMAN Q13126 5'-METHYLTHIOADENOSINE
PHOSPHORYLASE ;, mRNA sequence.

ACCESSION BF431095
VERSION BF431095.1 GI:11443209
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 205)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 205
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3573452"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo.

ORIGIN

Query Match 98.7%; Score 121.4; DB 2; Length 205;
Best Local Similarity 99.2%; Pred. No. 2e-28;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGCTTTAAGACCCCTGAAAGAAACCGCTAATAAGCCAAAGCTTA 60
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DB 157 GTTTCGGTGACCGGGCTATTAAAGACCCCTGAAAGAAACGCTAATAAGCCAAAGCTTA 98

QY 61 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTCAGAAACCTCCATTAACCTG 120
|||
DB 97 CTGCTCACTACCATACCTCAGATAGGGTCCACAGATGTCAGAAACCTCCATTAACCTG 38

QY 121 AAG 123
|||
DB 37 AAG 35

RESULT 14
AI919501 257 bp mRNA linear EST 14-DEC-1999
LOCUS AI919501/c
DEFINITION tp22b01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2188489 3'
similar to SW:MTAP HUMAN Q13126 5'-METHYLTHIOADENOSINE
PHOSPHORYLASE ;, mRNA sequence.

ACCESSION AI919501
VERSION AI919501.1 GI:5639356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 257)
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 246.
Location/Qualifiers
1. 257
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2188489"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN

Query Match 98.7%; Score 121.4; DB 1; Length 257;
Best Local Similarity 99.2%; Pred. No. 2.1e-28;

Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAAGCTTA 60
|||
Db 242 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAAGCTTA 183
QY 61 CTGCTCACTACCATACCTCAGATAGAGGTCCACGAATGTCAGAAACCTCCATAACCTG 120
|||
Db 182 CTGCTCACTACCATACCTCAGATAGAGGTCCACGAATGTCAGAAACCTCCATAACCTG 123
QY 121 AAG 123
|||
Db 122 AAG 120

RESULT 15
BG501032 728 bp mRNA linear EST 27-MAR-2001
LOCUS 602546438F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668825 5',
DEFINITION mRNA sequence.
ACCESSION BG501032
VERSION BG501032
KEYWORDS BG501032.1 GI:13462549
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1479 row: 1 column: 10
High quality sequence stop: 722.
Location/Qualifiers

FEATURES
source 1..728
location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4668825"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI
(ggccatctggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 98.7%; Score 121.4; DB 4; Length 728;
Best Local Similarity 99.2%; Pred. No. 2.5e-28;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAAGCTTA 60
|||
Db 489 GTTTCGGTGACCGGGTCTTAAAGACCCCTGAAGAAAGCGCTAATAAGCCAAAAGCTTA 548

QY 61 CTGCTCACTACCATACCTCAGATAGAGGTCCACGAATGGTCAGAAACCTCCATAACCTG 120
|||
Db 549 CTGCTCACTACCATACCTCAGATAGAGGTCCACGAATGGTCAGAAACCTCCATAACCTG 608
QY 121 AAG 123
|||
Db 609 AAG 611

Search completed: February 1, 2005, 14:58:30
Job time : 1383.94 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:48:48 ; Search time 1067.55 Seconds
(without alignment)
8416.542 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953

Perfect score: 190

Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGAATTGTTACGCAA 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_hcg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_by:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	190	100.0	567	9	AH013410S6	L42632 Homo sapien
2	190	100.0	849	9	CR541710	CR541710 Homo sapi
3	190	100.0	852	9	CR541670	CR541670 Homo sapi
4	190	100.0	870	6	AX826996	AX826996 Sequence
5	190	100.0	1021	9	L40432	L40432 Homo sapien
6	190	100.0	1450	6	AR474055	AR474055 Sequence
7	190	100.0	2269	9	HSU22333	U22233 Human methy
8	190	100.0	2763	6	AR059583	AR059583 Sequence
9	190	100.0	2763	6	I28320	I28320 Sequence 1
10	190	100.0	2763	6	AR473576	AR473576 Sequence
11	190	100.0	2763	6	AR474046	AR474046 Sequence
12	190	100.0	3083	6	AR144466	AR144466 Sequence
13	190	100.0	3083	6	AR342446	AR342446 Sequence
14	190	100.0	168656	9	AL359922	AL359922 Human DNA
15	190	100.0	250000	9	AB060808	AB060808 Homo sapi
16	188.4	99.2	1890	9	BC026106	BC026106 Homo sapi
17	164.4	86.5	807	9	L42635	L42635 Homo sapien
18	164.4	86.5	94125	9	AC016966	AC016966 Homo sapi
19	164.4	86.5	168366	2	AC069409	AC069409 Homo sapi

C	20	164.4	86.5	180606	2	AC073406	AC073406 Homo sapi
C	21	154.8	81.5	1055	10	AB056100	AB056100 Mus muscu
C	22	154.8	81.5	2565	10	BC003858	BC003858 Mus muscu
C	23	154.8	81.5	194025	10	AL831719	AL831719 Mouse DNA
C	24	148.4	78.1	225782	2	AC109529	AC109529 Rattus no
C	25	148.4	78.1	287775	2	AC108638	AC108638 Rattus no
C	26	119	62.6	441	6	CQ461249	CQ461249 Sequence
C	27	106.8	56.2	1255	5	BC056545	BC056545 Danio rer
C	28	106.8	56.2	1265	5	BC046035	BC046035 Danio rer
C	29	106.8	56.2	150073	5	BX323448	BX323448 Zebrafish
C	30	106.8	56.2	161859	2	CR385087	CR385087 Danio rer
C	31	97	51.1	339	9	AF216650	AF216650 Homo sapi
C	32	96.6	50.8	230762	2	AC097556	AC097556 Rattus no
C	33	96.6	50.8	232771	2	AC128406	AC128406 Rattus no
C	34	94.2	49.6	170899	2	AC144208	AC144208 Macaca mu
C	35	86.8	45.7	1193	6	CQ581994	CQ581994 Sequence
C	36	86.8	45.7	1227	3	BT004912	BT004912 Drosophi1
C	37	86.8	45.7	3322	6	CQ581993	CQ581993 Sequence
C	38	86.8	45.7	3511	6	CQ586454	CQ586454 Sequence
C	39	86.8	45.7	52465	2	AC020084	AC020084 Drosophi1
C	40	86.8	45.7	161244	3	AC009535	AC009535 Drosophi1
C	41	86.8	45.7	175506	3	AC008004	AC008004 Drosophi1
C	42	86.8	45.7	290783	3	AE003803	AE003803 Drosophi1
C	43	75.8	39.9	90801	9	AC025033	AC025033 Homo sapi
C	44	75.8	39.9	146349	2	AC012027	AC012027 Homo sapi
C	45	75.8	39.9	171615	2	AC089988	AC089988 Homo sapi

ALIGNMENTS

RESULT 1	AH013410S6	567 bp	DNA	linear	PRI 01-DEC-2003
LOCUS	AH013410S6	567 bp	DNA	linear	PRI 01-DEC-2003
DEFINITION	Homo sapiens methylthioadenosine phosphorylase (MTAP) gene, exon 6.				
ACCESSION	L42632				
VERSION	L42632.1	GI:38570312			
KEYWORDS					
SEGMENT	6 of 8				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L. and Carson,D.A.				
TITLE	Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)				
MEDLINE	96234115				
PUBMED	8650244				
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	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/chromosome="9"				
	/map="9p22-p21"				
	/clone="p1-267"				
	/tissue_type="placenta"				
	64..303				
	/gene="MTAP"				
	/note="putative"				
	/number=6				
ORIGIN					
	Query Match	100.0%;	Score 190;	DB 9;	Length 567;
	Best Local Similarity	100.0%;	Pred. No. 2.5e-49;		
	Matches 190;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 GTTCTTATAGAGACTGCTAAGACTAGAGACTCCGGTCCACTCAAGGGGACAATGTC 60				
DB	64 GTTCTTATAGAGACTGCTAAGACTAGAGACTCCGGTCCACTCAAGGGGACAATGTC 123				

QY 61 ACAATCGAGGACCTCGTTTACGTCGCCGACAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 124 ACAATCGAGGACCTCGTTTACGTCGCCGACAGAAAGCTTCATGTTCCGCACCTGGGG 183
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGCTGAATT 180
|||||
Db 184 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGCTGAATT 243
QY 181 TGTTACGCAA 190
|||||
Db 244 TGTTACGCAA 253

RESULT 2
CR541710
LOCUS 849 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834H1128D for
gene MTAP, methylthioadenosine phosphorylase; complete cds, without
stopcodon.
CR541710
VERSION CR541710.1 GI:49456380
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 849)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
Unpublished
2 (bases 1 to 849)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT RZPD; RZPD0834H1128D, ORFNO 3404
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H1128D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
834
www.rzpd.de/cgi-bin/products/showlib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131058.01L
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found
AA exchange(s) at position (first base of changed triplet):
133(Leu->ser) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/
Location/Qualifiers
1. .849

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834H1128D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5alpha"
/note="Vector: pDONR201, site_1: attPl; site_2: attp2"
1. .849
/gene="MTAP"
1. .>849
/gene="MTAP"
/codon_start=1
/protein_id="CAG46511.1"
/db_xref="GI:49456381"
/translation="MASGTTTAVKIGITGGLDDPEILEGRTEKYVDTPFGKPSDA
SLGKIKNVDVILARHGRQHTIMPSKVNYQANIMALKEGCTHIVTTACGSIREEI
QPGDIVIIDQFIDRTMRPQSFYDGSWSCARGVCHIPMAEPFCPTREVLLETKRLG
LRCHSKGTMTVTEGPRFSSRAESFMFRTWGADVIMTTVPEVVLAKKAGICVYSIAMA
TDYDCWKEHEEAVSVDRVLTLLKENANKAKSLTLTTPQIGSTEWSETLHNLKMAQF
SVLIPRH"

ORIGIN
Query Match 100.0%; Score 190; DB 9; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGAGACAATGTC 60
|||||
Db 451 GTTCTTAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGAGACAATGTC 510
QY 61 ACAATCGAGGACCTCGTTTACGTCGCCGACAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 511 ACAATCGAGGACCTCGTTTACGTCGCCGACAGAAAGCTTCATGTTCCGCACCTGGGG 570
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGCTGAATT 180
|||||
Db 571 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGCTGAATT 630
QY 181 TGTTACGCAA 190
|||||
Db 631 TGTTACGCAA 640

RESULT 3
CR541670
LOCUS 852 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834G1127D for
gene MTAP, methylthioadenosine phosphorylase; complete cds, incl.
stopcodon.
CR541670
VERSION CR541670.1 GI:49456300
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 852)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
Unpublished
2 (bases 1 to 852)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
COMMENT RZPD; RZPD0834G1127D, ORFNO 3305
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834G1127D RZPDLIB;

Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834
www.rzpd.de/cgi-bin/products/showlib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.

This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_002451 (GI:6006025) we found
AA exchange(s) at position (first base of changed triplet):
139(Leu->met) 166(ile->val)
Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES

source

1. .852
location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="RZPD0834G1127D"

/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"

/lab_host="DH5Alpha"

/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"

gene

1. .852
/gene="MTAP"

CDS

1. .852
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/codon_start=1

/protein_id="CAG46471.1"

/db_xref="GI:49456301"

/translation="MASGTTTAVKIGIGTGLDPEILLEGRTKXVNDTPFKPSDA
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QPGDIVIIDQFIDRTMRPQSFYDGSHCARGVCHIPMAEPFCPTREVLIEAKKLG
LRCHSKGTMTIEGPRSSRAESFMFRTMGADVIMNTVEVLAKAGICVASTAMA
TDYDCWKEHEAVSVDRVLTLEKNANKAKSLLTITPQIGSTWSETLHNLKMAQF
SVLLPRH"

ORIGIN

Query Match 100.0%; Score 190; DB 9; Length 852;
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGTC 60
|||||
Db 451 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGTC 510
QY 61 ACAATCGAGGAGCTGTTTAGCTCCGGGCAGAAAGCTTCATGTTCCGCACTGGGG 120
|||||
Db 511 ACAATCGAGGAGCTGTTTAGCTCCGGGCAGAAAGCTTCATGTTCCGCACTGGGG 570
QY 121 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTCTAAGAGGCTGAATT 180
|||||
Db 571 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTCTAAGAGGCTGAATT 630
QY 181 TGTACGCAA 190
|||||
Db 631 TGTACGCAA 640

RESULT 4
AX826996
LOCUS

AX826996 870 bp DNA linear PAT 12-DEC-2003

DEFINITION Sequence 1 from Patent WO03074083.

ACCESSION AX826996
VERSION AX826996.1 GI:39837205

KEYWORDS

SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Bloom,L.A., Boritzki,T.J., Kung,P.P., Ogden,R.C., Skaltzky,D.J.,
Zehnder,L.R., Kuhn,L.A. and Meng,J.J.

TITLE

Combination therapies for treating methylthioadenosine
phosphorylase deficient cells

Patent: WO 03074083-A 1 12-SEP-2003;
PFIZER INC. (US)

JOURNAL

FEATURES

source

1. .870
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Cloned MTAP cDNA"

ORIGIN

Query Match 100.0%; Score 190; DB 6; Length 870;
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGTC 60
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Db 457 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGTC 516
QY 61 ACAATCGAGGAGCTGTTTAGCTCCGGGCAGAAAGCTTCATGTTCCGCACTGGGG 120
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Db 517 ACAATCGAGGAGCTGTTTAGCTCCGGGCAGAAAGCTTCATGTTCCGCACTGGGG 576
QY 121 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTCTAAGAGGCTGAATT 180
|||||
Db 577 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTCTAAGAGGCTGAATT 636
QY 181 TGTACGCAA 190
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Db 637 TGTACGCAA 646

RESULT 5

LOCUS

L40432 1021 bp mRNA linear PRI 12-DEC-2000
DEFINITION Homo sapiens methylthioadenosine phosphorylase (MTAP) mRNA,
complete cds.

ACCESSION

L40432
VERSION L40432.1 GI:11602391

KEYWORDS

SOURCE
ORGANISM
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1021)
Nobori,T., Takabayashi,K., Tran,P., Orvis,L., Batova,A., Yu,A.L.

AUTHORS

TITLE

Genomic cloning of methylthioadenosine phosphorylase: a purine
metabolic enzyme deficient in multiple different cancers

Proc. Natl. Acad. Sci. U.S.A. 93 (12), 6203-6208 (1996)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

Direct Submission
Submitted (09-SEP-1996) The Sam and Rose Stein Institute for
Research on Aging, and Department of Medicine, University of
California at San Diego, La Jolla, CA 92093-0663, USA

COMMENT

GSDB:S:39613.
[Flatfile retrieved from GSDB Thu Dec 7 15:18:48 2000].

FEATURES

location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p22-p21"
/tissue_type="placenta"
/tissue_1ib="lambda gt11"
1..1021
/gene="MTAP"
111..962
/gene="MTAP"
/EC_number="2.4.2.28"
/note="putative"
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/protein_id="AG38871.1"
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/translation="MASGTTTAVKIGIGTGIDDEILEGRTEKYVDPFGKPSDA
LILGKIKNVDCVLARHGROHTIMPSKVNQANIMWALKEEGCTHIVTTACSLREEI
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LRCHSKGTMTVIEGPRFSSRAESFMRTWGADVIMTTVPEVVLAKIAGICYASIAMG
TDYDCWKEHEEAVSVDRVLTIKENANKAKSLTLTTIPQIGSTEMSETLHNLKNMAQF
SVLLPRH"

ORIGIN
Query Match 100.0%; Score 190; DB 9; Length 1021;
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGTC 60
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Db 561 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGTC 620
QY 61 ACAATCGAGGGACCTCGTTTACGCTCCGGGACAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 621 ACAATCGAGGGACCTCGTTTACGCTCCGGGACAGAAAGCTTCATGTTCCGCACCTGGGG 680
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTTGTTCTTGCTAAGAGGCTGGAATT 180
|||||
Db 681 GCGGATGTTATCAACATGACCAAGTTCAGAGGTTGTTCTTGCTAAGAGGCTGGAATT 740
QY 181 TGTTCAGCAA 190
|||||
Db 741 TGTTCAGCAA 750

RESULT 6
AR474055
LOCUS AR474055 1450 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 23 from patent US 6689864.
ACCESSION AR474055
VERSION AR474055.1 GI:42712808
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1450)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Cyclin dependent kinase 4 inhibitor
JOURNAL Patent: US 6689864-A 23 10-FEB-2004;
FEATURES
source location/Qualifiers
1..1450
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 1450;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGTC 60
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Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGACCTCGTTTACGCTCCGGGACAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGACCTCGTTTACGCTCCGGGACAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTTGTTCTTGCTAAGAGGCTGGAATT 180
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Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTTGTTCTTGCTAAGAGGCTGGAATT 1143
QY 181 TGTTCAGCAA 190
|||||
Db 1144 TGTTCAGCAA 1153

RESULT 7
HSU22233
LOCUS HSU22233 2269 bp mRNA linear PRI 25-NOV-1995
DEFINITION Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds.
ACCESSION U22233
VERSION U22233.1 GI:847723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2269)
Olopade,O.I., Pomyskala,H.M., Hagos,F., Sveen,L.W., Espinosa,R. III,
Dreyling,M.H., Gursky,S., Stadler,W.M., Le Beau,M.M. and
Bohlender,S.K.
Construction of a 2.8-megabase yeast artificial chromosome contig
and cloning of the human methylthioadenosine phosphorylase gene
from the tumor suppressor region on 9p21
Proc. Natl. Acad. Sci. U.S.A. 92 (14), 6489-6493 (1995)
7604019
MEDLINE
PUBMED
95327672
REFERENCE 2 (bases 1 to 2269)
Olopade,O.I.
Direct Submission
Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,
University of Chicago Pritzker School of Medicine, 5841 S. Maryland
Avenue, Chicago, IL 60637-1470, USA
location/Qualifiers
1..2269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"
/clone="18-11 cDNA"
/sex="male"
/cell_line="primary culture"
/cell_type="fibroblast"
/tissue_type="epidermis"
1..2269
/gene="MTAP"
122..973
CDS
122..973
/gene="MTAP"
/codon_start=1
/product="methylthioadenosine phosphorylase"
/protein_id="AAA81646.1"
/db_xref="GI:847724"

TITLE
JOURNAL
MEDLINE
PUBMED
95327672
REFERENCE 2 (bases 1 to 2269)
Olopade,O.I.
Direct Submission
Submitted (06-MAR-1995) Olufunmilayo I. Olopade, Medicine,
University of Chicago Pritzker School of Medicine, 5841 S. Maryland
Avenue, Chicago, IL 60637-1470, USA
location/Qualifiers
1..2269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"
/clone="18-11 cDNA"
/sex="male"
/cell_line="primary culture"
/cell_type="fibroblast"
/tissue_type="epidermis"
1..2269
/gene="MTAP"
122..973
CDS
122..973
/gene="MTAP"
/codon_start=1
/product="methylthioadenosine phosphorylase"
/protein_id="AAA81646.1"
/db_xref="GI:847724"

ORIGIN
Query Match 100.0%; Score 190; DB 9; Length 2269;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGTC 60
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QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 60
|||||
Db 572 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 631
QY 61 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 632 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 691
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 180
|||||
Db 692 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 751
QY 181 TGTTCAGCAA 190
|||||
Db 752 TGTTCAGCAA 761
RESULT 8
AR059583 2763 bp DNA linear PAT 29-SEP-1999
LOCUS AR059583
DEFINITION Sequence 1 from patent US 5840505.
ACCESSION AR059583
VERSION AR059583.1 GI:5986033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carrera,C.J., Carson,D.A., Cottam,H.B. and Nobori,T.
TITLE Method for inhibiting adenylosuccinate synthetase activity in
JOURNAL methylchadenosine phosphorlyase deficient cells
FEATURES Patent: US 5840505-A 1 24-NOV-1998;
source 1. 2763
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 60
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Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 1023
QY 61 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 1143
QY 181 TGTTCAGCAA 190
|||||
Db 1144 TGTTCAGCAA 1153
RESULT 9
128320 128320 2763 bp DNA linear PAT 06-FEB-1997
LOCUS 128320
DEFINITION Sequence 1 from patent US 5571510.
ACCESSION 128320
VERSION 128320.1 GI:1819096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Nobori,T. and Carson,D.A.
TITLE Method for selective methionine starvation of malignant cells in

JOURNAL mammals
Patent: US 5571510-A 1 05-NOV-1996;
FEATURES Location/Qualifiers
source 1. 2763
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 60
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Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 1023
QY 61 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 1143
QY 181 TGTTCAGCAA 190
|||||
Db 1144 TGTTCAGCAA 1153
RESULT 11
AR474046
RESULT 10
AR473576 2763 bp DNA linear PAT 20-FEB-2004
LOCUS AR473576
DEFINITION Sequence 14 from patent US 6689561.
ACCESSION AR473576
VERSION AR473576.1 GI:42711901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Tumor suppressor gene and methods for detection of cancer,
JOURNAL monitoring of tumor progression and cancer treatment
FEATURES Patent: US 6689561-A 14 10-FEB-2004;
source 1. 2763
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 60
|||||
Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGACTCCGGTGCCACTCAAGGGGACAATGCTC 1023
QY 61 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGACCTCGTTTATAGCTCCCGGGCAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGGAATT 1143
QY 181 TGTTCAGCAA 190
|||||
Db 1144 TGTTCAGCAA 1153

LOCUS AR474046 2763 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 14 from patent US 6689864.
ACCESSION AR474046
VERSION AR474046.1 GI:42712799
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2763)
AUTHORS Carson,D.A. and Nobori,T.
TITLE Cyclin dependent kinase 4 inhibitor
JOURNAL Patent: US 6689864-A 14 10-FEB-2004;
FEATURES
source location/Qualifiers
1..2763
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 60
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Db 964 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 120
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Db 1024 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 1143
QY 181 TGTTCACGCAA 190
|||||
Db 1144 TGTTCACGCAA 1153

RESULT 12
ARI44466
LOCUS ARI44466 3083 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210917.
ACCESSION ARI44466
VERSION ARI44466.1 GI:15106333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3083)
AUTHORS Carson,D.A. and Carrera,C.J.
TITLE Method for suppressing multiple drug resistance in cancer cells
JOURNAL Patent: US 6210917-A 1 03-APR-2001;
FEATURES
source location/Qualifiers
1..3083
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 60
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Db 1764 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 1823
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 120
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Db 1824 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 1883
QY 121 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 180
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Db 1884 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 1943
QY 181 TGTTCACGCAA 190
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Db 1944 TGTTCACGCAA 1953

RESULT 13
AR342446
LOCUS AR342446 3083 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 25 from patent US 6576420.
ACCESSION AR342446
VERSION AR342446.1 GI:33737456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3083)
AUTHORS Carson,D.A., Schmid,M. and Carrera,C.J.
TITLE Method for early diagnosis of, and determination of prognosis in,
cancer
JOURNAL Patent: US 6576420-A 25 10-JUN-2003;
FEATURES
source location/Qualifiers
1..3083
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 190; DB 6; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 60
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Db 1764 GTTCTTATAGAGACTGCTTAAGAGCTAGGACTCCGGTCCCACTCAAAAGGGGACAATGTC 1823
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 120
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Db 1824 ACAATCGAGGAGCCTCGTTTAACTCCCGGCGAAGAAAGCTTCATGTTCCGCACCTGGGG 1883
QY 121 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 180
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Db 1884 GCGGATGTTATCAACATGACCAAGTTCACAGAGTGTTCTTGCTAAGAGGCTGGAATT 1943
QY 181 TGTTCACGCAA 190
|||||
Db 1944 TGTTCACGCAA 1953

RESULT 14
AL359922
LOCUS AL359922 16866 bp DNA linear PRI 17-JAN-2001
DEFINITION Human DNA sequence from clone RP11-70L8 on chromosome 9, complete
sequence.
ACCESSION AL359922
VERSION AL359922.10 GI:12191425
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 16866)
AUTHORS Laird,G.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT
On Jan 13, 2001 this sequence version replaced gi:11878000.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9> RP11-70L8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

This sequence is the entire insert of clone RP11-70L8 The true left end of clone RP11-14912 is at 118787 in this sequence. The true right end of clone RP11-47303 is at 73731 in this sequence.

FEATURES

Source

1..168656
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-70L8"
/clone_lib="RPCI-11.1"

misc_feature

98399..98416
/note="Single clone region. Assembly confirmed by restriction digest data."

misc_feature

98649..98718
/note="Single clone region. Assembly confirmed by restriction digest data."

misc_feature

157251..157348
/note="Single clone region. L1 repeat. Assembly confirmed by restriction digest data"

ORIGIN

Query Match 100.0%; Score 190; DB 9; Length 168656;

Best Local Similarity 100.0%; Pred. No. 2.1e-49;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 60

Db 112028 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 112087

QY 61 ACAATCGAGGACCTCGTTTACGCTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120

Db 112088 ACAATCGAGGACCTCGTTTACGCTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 112147

QY 121 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180

Db 112148 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 112207

QY 181 TGTTCAGCAA 190

Db 112208 TGTTCAGCAA 112217

RESULT 15

AB060808

LOCUS AB060808 250000 bp DNA linear PRI 26-APR-2002

DEFINITION Homo sapiens gene for p16/CDKN2A, complete cds.

ACCESSION AB060808

VERSION AB060808.1 GI:20330501

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 Kohno,T., Inoue,K., Kitagawa,Y., Hayashi,Y., Matsuo,Y.,
Mizoguchi,H. and Yokota,J.

TITLE

Prevalent Involvement of Illegitimate V(D)J Recombination in
Chromosome 9p21 Deletions in Lymphoid Leukemia

JOURNAL

2 (bases 1 to 250000)

REFERENCE

Yokota,J., Kohno,T., Inoue,K. and Kitagawa,Y.

AUTHORS

Submitted (25-APR-2001) Takashi Kohno, National Cancer Center
Research Institute, Biology Division; 1-1, Tsukiji 5-chome,
Chuo-ku, Tokyo 104-0045, Japan (E-mail:tkkohno@gan2.res.ncc.go.jp,
Tel:81-3-3542-2511(ex.4652), Fax:81-3-3542-0807)

JOURNAL

Unpublished

FEATURES

Source

1..250000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"

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192072..192221))

CDS

/gene="p16/CDKN2A"
complement(join(185617..185630,188290..188596,
192072..192221))

/gene="p16/CDKN2A"

/codon_start=1

/product="p16/CDKN2A"

/protein_id="BAB91133.1"

/db_xref="GI:20330502"

/translation="MEPAAGSSMEPSADWLTAAARGVEEVRALLBAGALPNAPNSY
GRRPIQVMGSAVVALELLHGAEPNCADPATLTPVPHDAREGFLDTLVILHRAGA
RLDVRDAMGRLPVDLAELGHRDVARYLRAAAGTRGSNHRIDAAEGPSDIPD"

ORIGIN

Query Match 100.0%; Score 190; DB 9; Length 250000;

Best Local Similarity 100.0%; Pred. No. 2e-49;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 60

Db 72028 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 72087

QY 61 ACAATCGAGGACCTCGTTTACGCTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 120

Db 72088 ACAATCGAGGACCTCGTTTACGCTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGGG 72147

QY 121 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180

Db 72148 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 72207

QY 181 TGTTCAGCAA 190

Db 72208 TGTTCAGCAA 72217

Search completed: February 1, 2005, 13:26:02
Job time : 1069.55 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 10:46:43 ; Search time 249.351 Seconds
(without alignments)
3999.945 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGGAATTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1:	geneseqn1980s:*
2:	geneseqn1990s:*
3:	geneseqn2000s:*
4:	geneseqn2001as:*
5:	geneseqn2001bs:*
6:	geneseqn2002as:*
7:	geneseqn2002bs:*
8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	870	10	ADC37133 Cloned me
2	190	100.0	2197	10	ADC30327 Human nov
3	190	100.0	2763	2	AAT15167 Methylthi
4	190	100.0	2763	2	AAQ92813 Human MTA
5	190	100.0	2763	2	AAT85305 Human met
6	190	100.0	2763	2	AAZ00866 Human MTA
7	190	100.0	2763	5	AAF86091 Methylthi
8	190	100.0	2763	10	AAD64097 Human met
9	190	100.0	2784	2	AAQ99202 Pseudomon
10	190	100.0	3083	2	AAZ58284 Human met
11	190	100.0	3083	8	ABX10818 DNA encod
12	148	77.9	1419	10	AAD64106 CDK41 rel
13	135.2	71.2	662	6	ABQ59125 Human col
14	119	62.6	441	6	ABL81049 Human ova
15	86.8	45.7	1193	4	ABL08341 Drosophill
16	86.8	45.7	3322	4	ABL08340 Drosophill
17	86.8	45.7	3511	4	ABL11314 Drosophill
18	71.4	37.6	6461	4	ABL11024 Drosophill
19	59.8	31.5	300	2	AAZ14961 Human gen
20	59.6	31.4	110000	12	ADN46845_16 Continuation (17 o
21	59.6	31.4	110000	12	ADN46845_17 Continuation (18 o

22	59.6	31.4	110000	12	ADN47591_03 Continuation (4 of
23	59.6	31.4	110000	12	ADN46123_16 Continuation (17 o
24	59.6	31.4	110000	12	ADN46123_17 Continuation (18 o
25	59.6	31.4	110000	12	ADN47209_03 Continuation (4 of
26	59.6	31.4	110000	12	ADN46464_16 Continuation (17 o
27	59.6	31.4	110000	12	ADN46464_17 Continuation (18 o
28	59.6	31.4	110000	12	ADN47960_03 Continuation (4 of
29	58.8	30.9	790	2	AAZ16103 Human gen
30	57.2	30.1	349980	5	AAH41225 Pyrococu
31	54.6	28.7	110000	4	AAI99682_06 Continuation (7 of
32	54.6	28.7	110000	4	AAI99683_06 Continuation (7 of
33	53.2	28.0	596	10	ADG38065 Aspergill
34	53.2	28.0	1029	3	AAF14549 Aaf14549 Aspergill
35	50.2	26.4	349980	5	AAF86431 Pyrococu
36	47.8	25.2	110000	12	ADN46845_13 Continuation (14 o
37	47.8	25.2	110000	12	ADN47591_07 Continuation (8 of
38	47.8	25.2	110000	12	ADN46123_13 Continuation (14 o
39	47.8	25.2	110000	12	ADN47209_07 Continuation (8 of
40	47.8	25.2	110000	12	ADN46464_13 Continuation (14 o
41	47.8	25.2	110000	12	ADN47960_07 Continuation (8 of
42	41	21.6	110000	11	ADM27081 Hyperther
43	40	21.1	390	8	ABX41411 Bovine ES
44	39.6	20.8	404	8	ABZ54499 Aspergill
45	36.6	19.3	602	8	ABZ52169 Aspergill

ALIGNMENTS

RESULT 1	
ID	ADC37133 standard; cDNA; 870 BP.
XX	
AC	ADC37133;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Cloned methylthioadenosine phosphorylase, MTA, cDNA.
XX	
KW	combination therapy; methylthioadenosine phosphorylase; MTA; inhibitor;
KW	glycinamide ribonucleotide formyltransferase; GARFT;
KW	aminoimidazolecarboximide ribonucleotide formyltransferase; AICARFT;
KW	anti-toxicity agent; cell proliferative disorder; lung cancer; leukaemia;
KW	glioma; urothelial cancer; colon cancer; breast cancer; prostate cancer;
KW	pancreatic cancer; skin cancer; head; neck cancer; gene; ss.
XX	
OS	Unidentified.
XX	
PN	WO2003074083-A1.
XX	
PD	12-SEP-2003.
XX	
PF	17-FEB-2003; 2003WO-IB000615.
XX	
PR	04-MAR-2002; 2002US-0361645P.
PR	09-DEC-2002; 2002US-0432275P.
XX	
PA	(PFIZ) PFIZER INC.
XX	
PI	Bloom LA, Boritzki TJ, Kung P, Ogden RC, Skaltitzky DJ;
PI	Zehnder LR, Kuhn LA, Meng J;
XX	
DR	WPI; 2003-748252/70.
XX	
PT	Selectively killing methylthioadenosine phosphorylase deficient cells
PT	used for treating cell proliferative disorders comprises administering
PT	glycinamide ribonucleotide formyltransferase and anti-toxicity agent.
XX	
PS	Example 3B; Page 182-183; 189pp; English.
XX	
CC	This invention relates to novel combination therapies that selectively
CC	kill methylthioadenosine phosphorylase (MTAP) deficient cells. The
CC	combination therapies comprise administering an inhibitor of glycinamide

CC ribonucleotide formyltransferase (GARFT) and/or aminoimidazolecarboximide
CC ribonucleotide formyltransferase (AICARFT), and administering an anti-
CC toxicity agent during and after administration of the inhibitor. The
CC combination therapies can be used for selectively killing MTAP deficient
CC cells, and for treating cell proliferative disorders e.g. lung cancer,
CC leukaemia, glioma, urothelial cancer, colon cancer, breast cancer,
CC prostate cancer, pancreatic cancer skin cancer and head and neck cancer.
CC The anti-toxicity agent counteracts the toxicity of the inhibitor in the
CC MTAP-competent (i.e. healthy) cells and increases the maximally tolerated
CC dose of the inhibitor. This polynucleotide sequence represents the cloned
CC MTAP cDNA of the invention.

XX
SQ Sequence 870 BP; 247 A; 194 C; 224 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 190; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.6e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 60
Db |||||
457 GTTCTTATAGAGACTGCTAAGAAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 516
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db |||||
517 ACAATCGAGGAGCCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 576
QY 121 GCGGATGTTATCAACATGACCAAGTTCCAGAGGTGTTCTTCTAAGAGGCTGGAATT 180
Db |||||
577 GCGGATGTTATCAACATGACCAAGTTCCAGAGGTGTTCTTCTAAGAGGCTGGAATT 636
QY 181 TGTTCGCGAA 190
Db |||||
637 TGTTCGCGAA 646

RESULT 2
ADC30327
ID ADC30327 standard; cDNA; 2197 BP.

XX
AC ADC30327;

XX
DT 18-DEC-2003 (first entry)

XX
DE Human novel cDNA sequence, SEQ ID NO:409.

XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antilucer; osteopathic; immunosuppressive; antiinflammatory; cyostatic;
KW gene therapy; chromosome 3; gene; ss.

XX
OS Homo sapiens.

XX
PN WO2003029271-A2.

XX
PD 10-APR-2003.

XX
PF 24-SEP-2002; 2002WO-US030474.

XX
PR 24-SEP-2001; 2001US-0324631P.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;

PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;

XX
PI Haley-Vicence D, Drmanac RT;

DR
DR WPI; 2003-371981/35.

XX
DR P-PSDB; ADC31298.

PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.

PS Claim 1; SEQ ID NO 409; 1185bp; English.

XX
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 2197 BP; 718 A; 379 C; 471 G; 629 T; 0 U; 0 Other;

Query Match 100.0%; Score 190; DB 10; Length 2197;
Best Local Similarity 100.0%; Pred. No. 2.2e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 60
Db |||||
511 GTTCTTATAGAGACTGCTAAGAAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 570

QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db |||||
571 ACAATCGAGGAGCCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 630

QY 121 GCGGATGTTATCAACATGACCAAGTTCCAGAGGTGTTCTTCTAAGAGGCTGGAATT 180
Db |||||
631 GCGGATGTTATCAACATGACCAAGTTCCAGAGGTGTTCTTCTAAGAGGCTGGAATT 690

QY 181 TGTTCGCGAA 190
Db |||||
691 TGTTCGCGAA 700

RESULT 3
AAT15167
ID AAT15167 standard; DNA; 2763 BP.

XX
AC AAT15167;

XX
DT 29-JUN-1996 (first entry)

XX
DE Methylthioadenosine-phosphorylase gene.

XX

KW Human; methylthioadenosine-phosphorylase; chromosome walking;
KW interferon-alpha; CDK4I; tumour suppressor; chromosome-9p21;
KW cyclin-dependent kinase-4-inhibitor; probe; primer; mutation; leukaemia;
KW melanoma; diagnostic; dysplastic nevus syndrome; glioma;
KW non-small cell lung carcinoma; cancer; gene therapy; antisense; ribozyme;
KW antibody; imaging; ss.
XX
OS Homo sapiens.
FH Key
FT exon 254..421
FT exon /*tag= b
FT intron 422..615
FT intron /*tag= c
FT exon 616..720
FT exon /*tag= d
FT intron 721..963
FT intron /*tag= e
FT exon 964..1203
FT exon /*tag= f
XX
PN WO9528169-A1.
XX
PD 26-OCT-1995.
XX
PF 12-APR-1995; 95WO-US004655.
XX
PR 14-APR-1994; 94US-00227800.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Nobori T;
XX
DR WPI; 1995-373630/48.
XX
XX Cyclin dependent kinase inhibitor gene, related vectors and antibodies -
PT useful for diagnosis, assessing predisposition and treatment of cancers.
XX
XX Example 1; Page 96-101; 129pp; English.
PS
XX The sequence encodes a methylthioadenosine-phosphorylase, and is located
CC at chromosome-9p21. A cyclin-dependent protein-kinase-4-inhibitor (CDK4I)
CC tumour suppressor gene (AAT15157-58) is located between this gene and an
CC interferon-alpha gene cluster, and has been isolated by chromosome
CC walking. The CDK4I gene, probe and primer derivatives and the gene
CC product may be used in diagnosis of cancer, particularly melanoma
CC (especially dysplastic nevus syndrome), glioma, non-small cell lung
CC carcinoma or leukaemia. The gene may also be used in cancer gene therapy,
CC or in antitumour antisense oligonucleotide or ribozyme construction.
CC Antibodies against CDK4I may be used in diagnosis or in vivo imaging
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;
Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGGTC 1023

QY 61 ACAATCGAGGAGACTCGTTTACGCTCCGGGCAAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db 1024 ACAATCGAGGAGACTCGTTTACGCTCCGGGCAAGAAAGCTTCATGTTCCGCACCTGGGG 1083

QY 121 GCGGATGTTATCAACATGACCAACAGTTCACAGAGGTGTTCTTGCTAAGAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCAACAGTTCACAGAGGTGTTCTTGCTAAGAGAGGCTGAATT 1143

QY 181 TGTTCAGCAA 190
Db 1144 TGTTCAGCAA 1153

RESULT 4
AAQ92813
ID AAQ92813 standard; DNA; 2763 BP.
XX
AC AAQ92813;
XX
DT 25-MAR-2003 (revised)
DT 05-DEC-1995 (first entry)
XX
XX Human MTase.
DE
XX
KW MTase; methyladenosine-phosphatase; malignancy; ss.
XX
OS Homo sapiens.
FH Key
FT exon 254..421
FT exon /*tag= a
FT exon 616..720
FT exon /*tag= b
FT exon 964..1203
FT exon /*tag= c
FT exon 1640..1762
FT exon /*tag= d
FT exon 2272..2310
FT exon /*tag= e
XX
PN WO9518233-A1.
XX
PD 06-JUL-1995.
XX
PF 22-DEC-1994; 94WO-US014920.
XX
PR 29-DEC-1993; 93US-00176855.
XX
PA (REGC) UNIV CALIFORNIA.
PA (CIBA) CIBA GEIGY CORP.
XX
PI Nobori T, Carson DA, Takabayashi K;
XX
DR WPI; 1995-246398/32.
XX
XX Detecting methyl:adenosine phosphatase in mammalian cells - by
PT hybridisation with specific oligonucleotide for detecting malignancy,
PT also new nucleic acid, expression vectors, derived polypeptide(s) and
PT antibodies.
XX
PS Claim 8; Page 34-35; 47pp; English.
XX
CC A cosmid gene library constructed from human placenta DNA was screened
CC using a MTase cDNA probe to isolate a human MTase genomic clone (sequence
CC given in AAQ92813). Absence of MTase from a cell is indicative of
CC malignancy. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2763 BP; 778 A; 501 C; 602 G; 805 T; 0 U; 77 Other;
Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTGCCACTCAAGGGGACAATGGTC 1023

QY 61 ACAATCGAGGAGACTCGTTTACGCTCCGGGCAAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db 1024 ACAATCGAGGAGACTCGTTTACGCTCCGGGCAAGAAAGCTTCATGTTCCGCACCTGGGG 1083

QY 121 GCGGATGTTATCAACATGACCAACAGTTCACAGAGGTGTTCTTGCTAAGAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCAACAGTTCACAGAGGTGTTCTTGCTAAGAGAGGCTGAATT 1143

XX Takabayashi K, Carson DA, Nobori T;
XX
XX WPI; 1999-507775/42.
XX
XX
PT Detecting catalytically active and inactive methylthioadenosine
PT phosphorylase (MTase) in mammalian cells useful for identifying malignant
PT cells which are suitable targets for methionine (MET) starvation therapy.
XX
XX Claim 6; Fig 1; 14pp; English.
XX
XX This invention describes a novel method for detecting catalytically
CC active and inactive methylthioadenosine phosphorylase (MTase) in
CC mammalian cells, using oligonucleotide probes which hybridize to MTase
CC nucleic acid coding regions. Detection of MTase encoding nucleic acid
CC indicates the cell has catalytically active MTase. The method is useful
CC for detecting malignant cells with a deficient MTase gene, useful for
CC identifying malignant cells which are suitable targets for methionine
CC (MET) starvation therapy. The new method is simple, efficient and
CC successful at determining MTase negative cells, unlike prior art
CC techniques, which include analysis of catalytic activity in cell
CC cultures, requiring a commercially unavailable radiochemical substrate,
CC and immunoassays, using MTase antibodies which are unable to be produced
CC in sufficient quantities. Recombinant MTase protein produced using the
CC new polynucleotide and vector, allows greater and purer production of
CC MTase than prior art techniques (using the Rangione method) for isolating
CC native MTase. This sequence represents human MTase encoding DNA which is
CC used in the method of the invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAGTAGAGACTCCGGTGCCACTCAAAAGGGGACAATGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGTAGAGACTCCGGTGCCACTCAAAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTGTTTAGCTCCCGGAGAGAAAGCTTCATGTTCCGACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTGTTTAGCTCCCGGAGAGAAAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 1084 GCGGATGTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
Db 1144 TGTTACGCAA 1153

RESULT 7
AAF86091
ID AAF86091 standard; DNA; 2763 BP.
XX
XX AAF86091;
XX
DT 06-JUL-2001 (first entry)
XX
DE Methylthioadenosine phosphorylase.
XX
KW Methylthioadenosine phosphorylase; adenyly succinate synthetase; ASS;
KM cancer; ds.
XX
XX Unidentified.
OS
XX
XX US6214571-B1.
PN
XX
PD 10-APR-2001.
XX
PF 24-NOV-1998; 98US-00199137.
XX

PR 29-DEC-1993; 93US-00176855.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Carrera CJ, Carson DA, Cottam HB, Nobori T;
XX
XX WPI; 2001-315458/33.
XX
XX
PT Inhibiting adenine succinate synthetase (ASS) activity in
PT methylthioadenosine phosphorylase deficient cells of mammalian host
PT involves administering ASS inhibitor which depletes adenosine 5'
PT monophosphate in cells.
XX
XX Disclosure; Fig 1; 17pp; English.
XX
XX The present invention relates to inhibiting adenyly succinate synthetase
CC (ASS) activity in methylthioadenosine phosphorylase (MTase) deficient
CC cells of mammalian host. The invention may be used as a treatment for
CC cancer, especially breast and colon cancer
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 190; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAGTAGAGACTCCGGTGCCACTCAAAAGGGGACAATGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGTAGAGACTCCGGTGCCACTCAAAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTGTTTAGCTCCCGGAGAGAAAGCTTCATGTTCCGACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTGTTTAGCTCCCGGAGAGAAAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 1084 GCGGATGTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
Db 1144 TGTTACGCAA 1153

RESULT 8
AAD64097
ID AAD64097 standard; DNA; 2763 BP.
XX
XX AAD64097;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human methylthioadenosine phosphorylase (MTase) genomic DNA.
XX
KW Human; tumour suppressor gene; cyclin-dependent kinase 4 inhibitor;
KW CDK4I; cancer; gene therapy; methylthioadenosine phosphorylase; MTase;
KW ds.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT exon 254..421
FT /*tag= a
FT 422..615
FT intron /*tag= b
FT 616..720
FT exon /*tag= c
FT intron /*tag= d
FT 721..963
FT exon /*tag= e
FT 964..1203
FT /*tag= e
XX
XX US2003138928-A1.
XX

PD 24-JUL-2003.
XX
XX 18-JUL-2001; 2001US-00908671.
PF
XX 26-AUG-1997; 97US-00921954.
PR
XX
PA (CARS/) CARSON D A.
PA (NOBO/) NOBORI T.
XX
XX Carson DA, Nobori T;
XX
XX WPI; 2003-851737/79.
DR
XX
XX New isolated polynucleotide encoding cyclin-dependent kinase 4l, useful
PT for preparing a composition for diagnosing or treating cancer.
PT
XX
XX Example 1; SEQ ID NO 14; 46pp; English.
PS
XX The present invention relates to novel tumour suppressor genes, termed as
CC cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding
CC proteins. The polynucleotides are useful for preparing a composition for
CC diagnosing or treating cancer. Sequences of the invention are also useful
CC in gene therapy. The present sequence is human methylthiodenosine
CC phosphorylase (MTase) genomic DNA used in the exemplification of the
CC invention
XX
SQ Sequence 2763 BP; 780 A; 505 C; 598 G; 803 T; 0 U; 77 Other;

Query Match 100.0%; Score 190; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
DB 964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCATGTCCGCACCTGGGG 120
DB 1024 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCATGTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGAAGAGGCTGAATT 180
DB 1084 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGAAGAGGCTGAATT 1143
QY 181 TGTTCAGCAA 190
DB 1144 TGTTCAGCAA 1153

RESULT 9
AAQ99202
ID AAQ99202 standard; DNA; 2784 BP.
XX
XX AAQ99202;
AC
XX 07-MAR-1996 (first entry)
DT
XX
XX Pseudomonas putida methylthiodenosine-phosphorylase DNA.
DE
XX
XX Enzyme; MTase; L-Met-L-deamino-gamma-mercaptomethane-lyase;
KW chemotherapy; cancer therapy; methionine starvation; ss.
KW
XX
XX Pseudomonas putida.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..2763
FT /*tag= a
XX
XX WO9517908-A1.
XX
XX 06-JUL-1995.
PD
XX
XX 22-DEC-1994; 94WO-US014919.
PF

XX
PR 29-DEC-1993; 93US-00176413.
XX
XX (REGC) UNITV CALIFORNIA.
PA
XX Nobori T, Carson DA;
PI
XX WPI; 1995-246192/32.
DR
XX
XX Selective methionine starvation of methylthio:adenosine phosphorylase
PT negative tumour cells - used in chemotherapy of mammalian malignant
PT cells.
PT
XX
XX Disclosure; Page 27-28; 46pp; English.
PS
XX
XX Antigenic peptides may be generated from this sequence encoding
CC methyladenosine-phosphorylase, which are then used to generate antibodies
CC specific for MTase. The produced antibodies may be used in an immunoassay
CC for the detection of MTase
XX
XX Sequence 2784 BP; 781 A; 505 C; 598 G; 804 T; 0 U; 96 Other;

Query Match 100.0%; Score 190; DB 2; Length 2784;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
DB 964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCATGTTCGCCACCTGGGG 120
DB 1024 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCATGTTCGCCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGAAGAGGCTGAATT 180
DB 1084 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGAAGAGGCTGAATT 1143
QY 181 TGTTCAGCAA 190
DB 1144 TGTTCAGCAA 1153

RESULT 10
AAX58284
ID AAX58284 standard; DNA; 3083 BP.
XX
XX AAX58284;
AC
XX
XX 02-AUG-1999 (first entry)
DT
XX
XX Human methylthiodenosine phosphorylase genomic DNA.
DE
XX
XX Methylthiodenosine phosphorylase; MTase; human;
KW multiple drug resistance; multidrug resistance; cancer; leukaemia;
KW therapy; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 119..2876
FT /*tag= a
FT /note= "contains introns"
FT 119..151
FT exon
FT /*tag= b
FT /number= 1
FT 152..449
FT intron
FT /*tag= c
FT /number= 1
FT 450..536
FT exon
FT /*tag= d
FT /number= 2
FT 537..723
FT intron

FT	/*tag= e
FT	/number= 2
FT	724. .782
FT	/*tag= f
FT	/number= 3
FT	783. .898
FT	/*tag= g
FT	/number= 3
FT	899. .1067
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FT	/number= 4
FT	1068. .1377
FT	/*tag= i
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FT	1378. .1480
FT	/*tag= j
FT	/number= 5
FT	1481. .1763
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FT	/number= 5
FT	1764. .1953
FT	/*tag= l
FT	/number= 6
FT	1954. .2425
FT	/*tag= m
FT	/number= 6
FT	2426. .2548
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FT	/number= 7
FT	2549. .2837
FT	/*tag= o
FT	/number= 7
FT	2838. .2876
FT	/*tag= p
FT	/number= 8
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PN	WO9920791-A1.
XX	
XX	29-APR-1999.
XX	
PF	23-OCT-1998; 98WO-US022557.
XX	
PR	23-OCT-1997; 97US-00956657.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Carson DA, Cottam HB, Nobori T, Carrera CJ;
XX	
DR	WPI; 1999-302753/25.
XX	
PT	Suppression of multiple drug resistance in cells, for treatment of, e.g.
PT	leukemia's.
XX	
PS	Example 3; Page 42-44; 45pp; English.
XX	

This is the DNA sequence of a human methylthioadenosine phosphorylase (MTase) genomic DNA clone that was isolated from a cosmid gene library using an MTase cDNA probe. The encoded enzyme catabolises methylthioadenosine to adenine for endogenous salvage incorporation into the intracellular AMP pool. The invention relates to methods for treating and preventing the onset and maintenance of multiple drug resistance (MDR) in animals undergoing cancer chemotherapy. In the methods provided, cells are depleted of AMP and ATP and are thus unable to support P-glycoprotein activity. One method obtains a population of target cells from a host and assays for loss of MTase activity. MTase deficient cells are treated with a purine synthesis inhibitor, such as l-alanosine, which starves the cells of adenine and suppresses P-glycoprotein activity. The MTase deficient host cells are preferably primary tumour cells comprising small-cell lung cancer cells, acute lymphoblastic leukemia cells, glioma cells or urothelial tumor cells, preferably in humans. MTase competent cells are also treated for MDR with purine synthesis inhibitors. MTase competent and deficient cells are also treated for malignancy with other anti-cancer drugs. MTase sequence-specific oligonucleotides can be used

CC	to detect the presence or absence of MTase in malignant cell lines					
XX	Sequence	3083 BP; 745 A; 531 C; 595 G; 807 T; 0 U; 405 Other;				
	Query Match	100.0%; Score 190; DB 2; Length 3083;				
	Best Local Similarity	100.0%; Pred. No. 2.4e-55;				
	Matches 190; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 GTTCTATAGAGACTGCTAAGAAGCTAGACTCCCGTGCCACTCAAAAGGGGACATGCTC 60					
Dd	1764 GTTCTATAGAGACTGCTAAGAAGCTAGACTCCCGTGCCACTCAAAAGGGGACATGCTC 1823					
OY	61 ACAATCGAGGACCTCGTTTTTAGCTCCCGGCAGAAAGCTTCATGTTCGCCACTGGGGG 120					
Dd	1824 ACAATCGAGGACCTCGTTTTTAGCTCCCGGCAGAAAGCTTCATGTTCGCCACTGGGGG 1883					
OY	121 GCCGATGTTATCAACATGACCACAGTTCACAGAGTGTCTTGTGCTAAGGAGCTGAATT 180					
Dd	1884 GCCGATGTTATCAACATGACCACAGTTCACAGAGTGTCTTGTGCTAAGGAGGCTGAATT 1943					
OY	181 TGTTACGCAA 190					
Dd	1944 TGTTACGCAA 1953					
 RESULT 11 ABX10818						
ID	ABX10818 standard; DNA; 3083 BP.					
XX	AC	ABX10818;				
XX	DT	17-APR-2003 (first entry)				
XX	DNA encoding rat methylthioadenosine phosphorylase (MTase).					
DE	Rat; methylthioadenosine phosphorylase; MTase; detection;					
KW	Rangione method; gene; ds.					
XX	OS	Rattus sp.				
XX						
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FT	exon	119..151				
FT		/tag= a				
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FT	intron	152..449				
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FT		/number= 2				
FT	intron	537..723				
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FT	exon	724..782				
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FT		/number= 3				
FT	intron	783..898				
FT		/tag= b				
FT		/number= 3				
FT	exon	899..1066				
FT		/tag= a				
FT		/number= 4				
FT	intron	1067..1377				
FT		/tag= b				
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FT	exon	1378..1480				
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FT		/number= 5				
FT	exon	1764..1953				
FT		/tag= a				

FT /number= 6
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FT /*tag= b
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FT exon 2426. .2548
FT /*tag= a
FT /number= 7
FT intron 2549. .2837
FT /*tag= b
FT /number= 7
FT exon 2838. .2876
FT /*tag= a
FT /number= 8

US2002146695-A1.
10-OCT-2002.
09-FEB-2001; 2001US-00780114.
29-DEC-1993; 93US-00176855.
02-JUN-1995; 95US-00459343.
04-MAY-1998; 98US-00072914.
(NOBO/) NOBORI T.
(CARSON/) CARSON D A.
(TAKA/) TAKABAYASHI K.
Nobori T, Carson DA, Takabayashi K;
WPI; 2003-208976/20.

Detection of methylthioadenosine phosphorylase presence in mammalian cells, by adding to sample oligonucleotide probes capable of hybridizing to methylthioadenosine phosphorylase encoding nucleic acid.

Claim 7; Fig 1; 16pp; English.

The invention describes a method of detecting methylthioadenosine phosphorylase (MTase) comprising adding oligonucleotide probes hybridisable to MTase encoding nucleic acid to an assayable sample of cells, where the presence of the nucleic acid indicates the presence of the MTase in a cell. The inventive method is simple and efficient in detecting the presence of MTase in the mammalian cell. The availability of the recombinant MTase enables the production of highly pure material with greater ease and in greater quantities than was obtained using Rangione method for the isolation and purification of native MTase. This sequence encodes rat methylthioadenosine phosphorylase (MTase)

Sequence 3083 BP; 745 A; 532 C; 595 G; 807 T; 0 U; 404 Other;

Query Match 100.0%; Score 190; DB 8; Length 3083;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 60
Db 1764 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 1823
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGGCAGAAAGCTTCATGTTCGCCACCTGGGG 120
Db 1824 ACAATCGAGGAGCCTCGTTTAGCTCCCGGGCAGAAAGCTTCATGTTCGCCACCTGGGG 1883
QY 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 180
Db 1884 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 1943
QY 181 TGTTAGCGCA 190
Db 1944 TGTTAGCGCA 1953

RESULT 12

AAD64106
ID AAD64106 standard; DNA; 1419 BP.
XX
AC AAD64106;
XX
DT 12-FEB-2004 (first entry)
XX
DE CDK4I related DNA #9.
XX
KW Tumour suppressor gene; cyclin-dependent kinase 4 inhibitor; CDK4I;
KW cancer; gene therapy; ds.
XX
OS Unidentified.

US2003138928-A1.
24-JUL-2003.
18-JUL-2001; 2001US-00908671.
26-AUG-1997; 97US-00921954.
(CARSON/) CARSON D A.
(NOBO/) NOBORI T.
Carson DA, Nobori T;
WPI; 2003-851737/79.

New isolated polynucleotide encoding cyclin-dependent kinase 4I, useful for preparing a composition for diagnosing or treating cancer.

Disclosure; SEQ ID NO 23; 46pp; English.

The present invention relates to novel tumour suppressor genes, termed as cyclin-dependent kinase 4 inhibitor (CDK4I) genes and their corresponding proteins. The polynucleotides are useful for preparing a composition for diagnosing or treating cancer. Sequences of the invention are also useful in gene therapy. The present sequence is CDK4I related DNA

Sequence 1419 BP; 368 A; 263 C; 340 G; 411 T; 0 U; 37 Other;

Query Match 77.9%; Score 148; DB 10; Length 1419;
Best Local Similarity 96.8%; Pred. No. 7.5e-41;
Matches 184; Conservative 0; Mismatches 0; Indels 6; Gaps 3;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTC 60
Db 949 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACA--GTC 1006
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGGCAGAAAGCTTCATGTTCGCCACCTGGGG 120
Db 1007 ACAATCGAGGAGCCTCGTTTAGCTCCCGGGCAGAAAGCTTCATGTTCGCCACCT--GGG 1064
QY 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 180
Db 1065 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTG--ATT 1122
QY 181 TGTTAGCGCA 190
Db 1123 TGTTAGCGCA 1132

RESULT 13
ABQ59125
ID ABQ59125 standard; cDNA; 662 BP.
XX
AC ABQ59125;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:2820.

KX Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiagalingam A, Lewis ME;
XX
XX WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists
XX
SQ Sequence 662 BP; 171 A; 134 C; 148 G; 165 T; 0 U; 44 Other;
Query Match 71.2%; Score 135.2; DB 6; Length 662;
Best Local Similarity 90.1%; Pred. No. 1.6e-36;
Matches 173; Conservative 0; Mismatches 16; Indels 3; Gaps 3;
QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAAGGGGCAATGCTC 60
DB 194 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCNNTCAANGGGGCAATGCTC 253
QY 61 ACAATCGAGGACCTCGTTTAGCTCCCGGCGAGAAGCTTCATGTTCCGCACCTGGGG 120
DB 254 ACAATCGAGGACCTCG-TTTAGCTCCCGGCGAGAANGCTTCATGTTCCGCACCTGGGG 312
QY 121 GC-GGATGTTATCAACATGACCAACAGTCCAGAGGTGTTCTTGT-AAGAGGCTGAA 178
DB 313 GCNGATGTTATCAACATGACCAACANTTCAAGAGGTGGTTTGCTAAANGANGCTGAA 372
QY 179 TTTGTTACGCA 190
DB 373 TTTGATACGCA 384
RESULT 14
ID ABL81049 standard; cDNA; 441 BP.
XX
AC ABL81049;
XX
DT 17-MAY-2002 (first entry)

XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:4027.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017756.
XX
PR 26-MAY-2000; 2000US-0207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
PI
XX
XX WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX
PS Claim 1; SEQ ID NO 4027; 489pp; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
CC or antigen presenting cells that express (II). (I) has cytostatic
CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
CC detecting ovarian cancer in a patient's biological sample preferably
CC serum or ovarian tissue. The method comprises contacting a biological
CC sample from a patient with (IV), detecting the amount of polynucleotide
CC hybridising to (IV) and comparing the amount to a predetermined cutoff
CC value and thereby detecting ovarian cancer in the patient, where the
CC amount of polynucleotide hybridising to (IV) is detected preferably by
CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC useful for stimulating and/or expanding T cells specific for an ovarian
CC tumour protein comprising contacting T cells with (III) or (II). (III) is
CC useful in design and preparation of ribozyme molecules for inhibiting
CC expression of the tumour polypeptides and proteins in tumour cells; and
CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
CC library using well known techniques
XX
SQ Sequence 441 BP; 115 A; 100 C; 118 G; 107 T; 0 U; 1 Other;
Query Match 62.6%; Score 119; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.1e-31;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAAGGGGCAATGCTC 60
DB 323 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAAGGGGCAATGCTC 382
QY 61 ACAATGAGGAGACCTCGTTTAGCTCCCGGCGAGAAGCTTCATGTTCCGCACCTGGGG 119
DB 383 ACAATGAGGAGACCTCGTTTAGCTCCCGGCGAGAAGCTTCATGTTCCGCACCTGGGG 441
RESULT 15
ID ABL08341 standard; cDNA; 1193 BP.
XX
AC ABL08341;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19505.

```
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB64238.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Claim 1; SEQ ID NO 19505; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1193 BP; 306 A; 294 C; 296 G; 297 T; 0 U; 0 Other;
SQ
Query Match 45.7%; Score 86.8; DB 4; Length 1193;
Best Local Similarity 66.7%; Pred. No. 1.4e-19;
Matches 124; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 2 TTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGTCA 61
Db 793 TTCTGCTTCAGGCGCGCAAGAGAGCTGAGATTCCCGCCACGATTAAGGCCACCATTTGA 852
QY 62 CAATCGAGGGAGCCTCGTTTAACTCCGGGAGAAAGCTTCATGTTCGACCTGGGGG 121
Db 853 CTATTGAGGGTCCGCGCTTCTCCTTCGCTCGAGAGCCACATGTTCGTCAGTGGGCG 912
QY 122 CGATGTTATCAACATGACCAAGTTCAGAGAGTGTTCTTGTAAAGAGGCTGAATT 181
Db 913 GGGACCTCATTAACATGACCAAGTTCAGAGAGTGTTCTTGTAAAGAGGCTGGCTTAC 972
QY 182 GTTACG 187
Db 973 TTTACG 978
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%
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- 6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

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SUMMARIES

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2	190	100.0	2763	1 US-08-176-413-1	Sequence 1, Appl
3	190	100.0	2763	2 US-08-612-542B-1	Sequence 1, Appl
4	190	100.0	2763	2 US-08-772-113-1	Sequence 1, Appl
5	190	100.0	2763	3 US-09-199-137-1	Sequence 1, Appl
6	190	100.0	2763	4 US-08-227-800A-14	Sequence 14, Appl
7	190	100.0	2763	4 US-08-921-954-14	Sequence 14, Appl
8	190	100.0	2763	5 PCT-US94-14919-1	Sequence 1, Appl
9	190	100.0	2763	5 PCT-US94-14920-1	Sequence 1, Appl
10	190	100.0	3083	3 US-08-956-657-1	Sequence 25, Appl
11	190	100.0	3083	4 US-09-335-231-25	Sequence 25, Appl
12	86.8	45.7	1104	4 US-09-270-767-13253	Sequence 13253, A
13	54.6	28.7	4403765	3 US-09-103-840A-2	Sequence 2, Appl
14	54.6	28.7	4411529	3 US-09-103-840A-1	Sequence 1, Appl
15	39.8	20.9	738	4 US-09-248-796A-3979	Sequence 3979, Ap
16	34.8	18.3	849	4 US-09-134-000C-2607	Sequence 7, Appl
17	31.8	16.7	486	2 US-08-199-984-7	Sequence 35, Appl
18	30	15.8	2119	4 US-09-620-312D-35	Sequence 5706, Ap
19	29.6	15.6	1542	4 US-09-489-039A-5706	Sequence 1090, Ap
20	28.8	15.2	465	4 US-09-489-039A-1090	Sequence 1038, Ap
21	28.8	15.2	1278	4 US-09-489-039A-1038	Sequence 3980, Ap
22	28.4	14.9	600	4 US-09-248-796A-3980	Sequence 10435, A
23	28.4	14.9	987	4 US-09-252-991A-10424	Sequence 10435, A
24	28.4	14.9	1350	4 US-09-270-767-10435	Sequence 10517, A
25	28.4	14.9	1422	4 US-09-252-991A-10517	Sequence 10738, A
26	28.4	14.9	2133	4 US-09-252-991A-10738	Sequence 17, Appl
27	28.4	14.9	48974	3 US-08-920-422-17	

28	28	14.7	160	2 US-08-890-980-26	Sequence 26, Appl
29	28	14.7	160	3 US-08-890-979-26	Sequence 26, Appl
30	28	14.7	160	3 US-09-032-894-26	Sequence 26, Appl
31	28	14.7	160	3 US-09-031-626-26	Sequence 9, Appl
32	28	14.7	416	2 US-08-890-980-9	Sequence 9, Appl
33	28	14.7	416	3 US-08-890-979-9	Sequence 9, Appl
34	28	14.7	416	3 US-09-032-894-9	Sequence 9, Appl
35	28	14.7	416	3 US-09-031-626-9	Sequence 33, Appl
36	27.8	14.6	570	4 US-09-134-000C-33	Sequence 1498, Ap
37	27.8	14.6	876	4 US-09-107-532A-1498	Sequence 3296, Ap
38	27.6	14.5	957	4 US-09-489-039A-3296	Sequence 252, App
39	27.6	14.5	1260	4 US-09-489-039A-3298	Sequence 1, Appl
40	27.4	14.4	12848	3 US-09-453-702B-252	Sequence 1, Appl
41	27.4	14.4	1664976	4 US-08-916-421B-1	Sequence 106, App
42	27.4	14.4	1664976	4 US-09-692-570-1	Sequence 101, App
43	27.2	14.3	3058	3 US-08-818-112-106	Sequence 106, App
44	27.2	14.3	3058	3 US-08-818-111-101	Sequence 106, App
45	27.2	14.3	3058	3 US-09-056-556-106	

ALIGNMENTS

RESULT 1
US-08-921-954-23
; Sequence 23, Application US/08921954
; Patent No. 6689864
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; No. 6689864ori, Tsutomu
; TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
; Detection of Cancer, Monitoring of Tumor Progression and
; Cancer Treatment
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921, 954
; FILING DATE: 26-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/908, 671A
; FILING DATE: 18-Jul-2001
; APPLICATION NUMBER: US 08/921, 954
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hirsch, Matthew E.
; REGISTRATION NUMBER: 47,651
; REFERENCE/DOCKET NUMBER: 023070-104042US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1450
; OTHER INFORMATION: /note= "methylthiodenosine"

phosphorylase (MTase) genomic nucleotide
sequence"
FEATURE:
NAME/KEY: exon
LOCATION: 254..421
FEATURE:
NAME/KEY: exon
LOCATION: 616..720
FEATURE:
NAME/KEY: exon
LOCATION: 964..1203
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-921-954-23

Query Match 100.0%; Score 190; DB 4; length 1450;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTACGCTCCCGGACAGAAAGCTTCATGTTCCGACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTCGTTTACGCTCCCGGACAGAAAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTACGCAA 190
Db 1144 TGTACGCAA 1153

RESULT 2

US-08-176-413-1
Sequence 1, Application US/08176413
Patent No. 5571510
GENERAL INFORMATION:
APPLICANT: No. 5571510ori, Tsutomu
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE
TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,413
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD2864
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-08-176-413-1

Query Match 100.0%; Score 190; DB 1; length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCTCAAGGGGACAATGGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTACGCTCCCGGACAGAAAGCTTCATGTTCCGACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTCGTTTACGCTCCCGGACAGAAAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTACGCAA 190
Db 1144 TGTACGCAA 1153

RESULT 3

US-08-612-542B-1
Sequence 1, Application US/08612542B
Patent No. 5840505
GENERAL INFORMATION:
APPLICANT: Carrera, Carlos J.
APPLICANT: Coltam, Howard B.
APPLICANT: No. 5840505ori, Tsutomu
APPLICANT: Carson, Dennis A.
TITLE OF INVENTION: METHOD FOR INHIBITING ADENYLOSUCCINATE SYNTHETASE
TITLE OF INVENTION: ACTIVITY IN MALIGNANT METHYLTTHIOADENOSINE PHOSPHORYLASE DEFICI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,542B
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:

CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-08-612-542B-1

Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGTC 60
|||||
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGAGCCTCGTTTAGCTCCCGGAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
|||||
Db 1144 TGTTACGCAA 1153

RESULT 4

US-08-772-113-1
Sequence 1, Application US/08772113
Patent No. 5942393
GENERAL INFORMATION:
APPLICANT: No. 5942393ori, Tsutomu
APPLICANT: Carson, Dennis A.
APPLICANT: Takabayashi, Kenji
TITLE OF INVENTION: METHOD FOR DETECTION OF
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,113
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/176,855
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:

CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-08-772-113-1

Query Match 100.0%; Score 190; DB 2; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGTC 60
|||||
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 1024 ACAATCGAGGAGCCTCGTTTAGCTCCCGGAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
|||||
Db 1144 TGTTACGCAA 1153

RESULT 5

US-09-199-137-1
Sequence 1, Application US/09199137
Patent No. 6214571
GENERAL INFORMATION:
APPLICANT: No. 6214571ori, Tsutomu
APPLICANT: Carson, Dennis A.
APPLICANT: Carrera, Carlos J.
APPLICANT: Coltam, Howard B.
TITLE OF INVENTION: METHOD FOR DETECTION OF
TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,137
FILING DATE: 24-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,855
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD3057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
US-09-199-137-1

Query Match 100.0%; Score 190; DB 3; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCCACTCAAGGGGACAATGCTC 60
|||||
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCCACTCAAGGGGACAATGCTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCCGGAGAGAGCTTCATGTTCCGACCTGGGG 120
|||||
Db 1024 ACAATCGAGGAGCCTCGTTTAACTCCCGGAGAGAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 1084 GCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
|||||
Db 1144 TGTTACGCAA 1153

RESULT 6

US-08-227-800A-14
Sequence 14, Application US/08227800A
Patent No. 6689561
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: NOBORI, TSUTOMU
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
TITLE OF INVENTION: DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CANCER
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800A
FILING DATE: 14-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthioadenosine Phosphorylase (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 1..2763
US-08-227-800A-14

Query Match 100.0%; Score 190; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCCACTCAAGGGGACAATGCTC 60
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Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCCACTCAAGGGGACAATGCTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCCGGAGAGAGCTTCATGTTCCGACCTGGGG 120
|||||
Db 1024 ACAATCGAGGAGCCTCGTTTAACTCCCGGAGAGAGCTTCATGTTCCGACCTGGGG 1083
QY 121 GCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 1084 GCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTTACGCAA 190
|||||
Db 1144 TGTTACGCAA 1153

RESULT 7

US-08-921-954-14
Sequence 14, Application US/08921954
Patent No. 6689864
GENERAL INFORMATION:
APPLICANT: Carson, Dennis A.
APPLICANT: No. 6689864ori, Tsutomu
TITLE OF INVENTION: Tumor Suppressor Gene and Methods for
TITLE OF INVENTION: Detection of Cancer, Monitoring of Tumor Progression and
TITLE OF INVENTION: Cancer Treatment
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,954
FILING DATE: 26-Aug-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/908,671A
FILING DATE: 18-Jul-2001
APPLICATION NUMBER: US 08/921,954
FILING DATE: 20-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hirsch, Matthew E.
REGISTRATION NUMBER: 47,651
REFERENCE/DOCKET NUMBER: 023070-104042US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..2763

OTHER INFORMATION: /note= "full-length
methylthiodenosine phosphorylase
(MTase) genomic nucleotide sequence"
FEATURE:
NAME/KEY: exon
LOCATION: 254..421
FEATURE:
NAME/KEY: exon
LOCATION: 616..720
FEATURE:
NAME/KEY: exon
LOCATION: 964..1203
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-921-954-14

Query Match 100.0%; Score 190; DB 4; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTAGAGACTGCTAAGAGCTAGACTCCGGTCCACTCAAGGGGACAATGTC 60
|||
Db 964 GTTCTTAGAGACTGCTAAGAGCTAGACTCCGGTCCACTCAAGGGGACAATGTC 1023
|||
Qy 61 ACAATCGAGGACCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 120
|||
Db 1024 ACAATCGAGGACCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 1083
|||
Qy 121 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGAATT 180
|||
Db 1084 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGAATT 1143
|||
Qy 181 TGTACGCAA 190
|||
Db 1144 TGTACGCAA 1153
|||

RESULT 8

PCT-US94-14919-1

Sequence 1, Application PC/TUS9414919

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY

APPLICANT: OF CALIFORNIA

TITLE OF INVENTION: METHOD FOR SELECTIVE METHIONINE

TITLE OF INVENTION: STARVATION OF MALIGNANT CELLS IN MAMMALS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 N. Figueroa Street, 5th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14919

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berliner, Robert

REGISTRATION NUMBER: 20,121

REFERENCE/DOCKET NUMBER: 5555-286

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-977-1001

TELEFAX: 213-977-1003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2763 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: methyladenosine phosphatase
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14919-1

Query Match 100.0%; Score 190; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTTAGAGACTGCTAAGAGCTAGACTCCGGTCCACTCAAGGGGACAATGTC 60
|||
Db 964 GTTCTTAGAGACTGCTAAGAGCTAGACTCCGGTCCACTCAAGGGGACAATGTC 1023
|||
Qy 61 ACAATCGAGGACCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 120
|||
Db 1024 ACAATCGAGGACCTCGTTTAGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 1083
|||
Qy 121 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGAATT 180
|||
Db 1084 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGAATT 1143
|||
Qy 181 TGTACGCAA 190
|||
Db 1144 TGTACGCAA 1153
|||

RESULT 9

PCT-US94-14920-1

Sequence 1, Application PC/TUS9414920

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY

APPLICANT: OF CALIFORNIA

TITLE OF INVENTION: METHOD FOR DETECTION OF

TITLE OF INVENTION: METHYLTHIODENOSINE PHOSPHATASE DEFICIENCY IN MAMMALIAN

TITLE OF INVENTION: CELLS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 N. Figueroa Street, 5th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14920

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berliner, Robert

REGISTRATION NUMBER: 20,121

REFERENCE/DOCKET NUMBER: 5555-287

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213-977-1001

TELEFAX: 213-977-1003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2763 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: methyladenosine phosphatase

FEATURE:

NAME/KEY: CDS
LOCATION: 1..2763
PCT-US94-14920-1

Query Match 100.0%; Score 190; DB 5; Length 2763;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCACTCAAGGGGACAATGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCACTCAAGGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTCGTTTAGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGTAAAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGTAAAGAGGCTGAATT 1143
QY 181 TGTACGCAA 190
Db 1144 TGTACGCAA 1153

RESULT 10

US-08-956-657-1

Sequence 1, Application US/08956657

Patent No. 6210917

GENERAL INFORMATION:

APPLICANT: NO. 6210917ori et al., Tsutomu

TITLE OF INVENTION: METHOD FOR DETECTION OF

TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENCY IN MAMMOLIAN

TITLE OF INVENTION: CELLS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: U.S.A.

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,657

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/827,342

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,855

FILING DATE: 29-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/050001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3083 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-956-657-1

Query Match 100.0%; Score 190; DB 3; Length 3083;

Best Local Similarity 100.0%; Pred. No. 5.1e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCACTCAAGGGGACAATGTC 60
Db 1764 GTTCTTATAGAGACTGCTAAGAGCTAGAGCTCCGGTGCCACTCAAGGGGACAATGTC 1823
QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 120
Db 1824 ACAATCGAGGAGCCTCGTTTAGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 1883
QY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGTAAAGAGGCTGAATT 180
Db 1884 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTGTAAAGAGGCTGAATT 1943
QY 181 TGTACGCAA 190
Db 1944 TGTACGCAA 1953

RESULT 11

US-09-335-231-25

Sequence 25, Application US/09335231

Patent No. 6576420

GENERAL INFORMATION:

APPLICANT: Carson, Dennis A.

APPLICANT: Schmid, Mathias

APPLICANT: Carrera, Carlos J.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of

TITLE OF INVENTION: Prognosis in, Cancer

FILE REFERENCE: 023070-108010US

CURRENT APPLICATION NUMBER: US/09/335,231

CURRENT FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: US 60/090,411

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 25

LENGTH: 3083

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: genomic sequence for methylthioadenosine

OTHER INFORMATION: phosphorylase (MTAP) gene

NAME/KEY: modified_base

LOCATION: (1)..(3083)

OTHER INFORMATION: n = unknown

NAME/KEY: exon

LOCATION: (119)..(151)

OTHER INFORMATION: exon 1

NAME/KEY: exon

LOCATION: (450)..(536)

OTHER INFORMATION: exon 2

NAME/KEY: exon

LOCATION: (724)..(782)

OTHER INFORMATION: exon 3

NAME/KEY: exon

LOCATION: (899)..(1066)

OTHER INFORMATION: exon 4

NAME/KEY: exon

LOCATION: (1378)..(1480)

OTHER INFORMATION: exon 5

NAME/KEY: exon

LOCATION: (1764)..(1953)

OTHER INFORMATION: exon 6

NAME/KEY: exon

LOCATION: (2426)..(2548)

OTHER INFORMATION: exon 7

NAME/KEY: exon

LOCATION: (2838)..(2876)

OTHER INFORMATION: exon 8

US-09-335-231-25

Query Match 100.0%; Score 190; DB 4; Length 3083;
Best Local Similarity 100.0%; Pred. No. 5.1e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTCCCACTCAAGGGGACATGTC 60
DB 1764 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTCCCACTCAAGGGGACATGTC 1823
QY 61 ACAATCGAGGAGCTCTGTTTACCTCCGGGAGAAAGCTTCATGTTCCGCACTGGGG 120
DB 1824 ACAATCGAGGAGCTCTGTTTACCTCCGGGAGAAAGCTTCATGTTCCGCACTGGGG 1883
QY 121 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTAAAGAGGCTGAATT 180
DB 1884 GCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTAAAGAGGCTGAATT 1943
QY 181 TGTTCGCAA 190
DB 1944 TGTTCGCAA 1953

RESULT 12

US-09-270-767-13253
; Sequence 13253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13253
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13253

Query Match 45.7%; Score 86.8; DB 4; Length 1104;
Best Local Similarity 66.7%; Pred. No. 4.6e-22;
Matches 124; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 2 TTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTCCCACTCAAGGGGACATGTC 61
DB 538 TTCTGCTTCAAGCGGCGCAAGAGCTGAGATTCCCGCCACGATTAAGCCACATTGTA 597
QY 62 CAATCGAGGAGCTCTGTTTACCTCCGGGAGAAAGCTTCATGTTCCGCACTGGGG 121
DB 598 CTATTGAGGGTCCGCGCTTCTCTCTGCTCGAGAGCCACATGTTCCGTCAGTGGGG 657
QY 122 CGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTTGTAAAGAGGCTGAATT 181
DB 658 GGGAGCTCATTAACATGACCAACGTCGTCAGAGTGTGCTAGCCAGAGGCTGGCTTAC 717
QY 182 GTTACG 187
DB 718 TTTCACG 723

RESULT 13

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2

; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 28.7%; Score 54.6; DB 3; Length 4403765;
Best Local Similarity 61.7%; Pred. No. 1.7e-08;
Matches 87; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 49 GGGACATGTCACATCGAGGAGCTCTTTAGCTCCCGGAGAAAGCTTCATGTTTC 108
DB 628349 GGGACATGTCGTCATCCAGGGTCCGGTTTCCACCCCGGAGAAAGCCAGTGTTTC 628408
QY 109 CGACCTGGGGGGCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTGCTAAG 168
DB 628409 GCCGTCGGGGGTGTCATCTGTTCAACATGACCGGCTATCCGAGCGGTGCTGCTGCG 628468
QY 169 GAGGTGAATTGTTACGCA 189
DB 628469 GAACTCGAATTATGCTACGCA 628489

RESULT 14

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 28.7%; Score 54.6; DB 3; Length 4411529;
Best Local Similarity 61.7%; Pred. No. 1.7e-08;
Matches 87; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 49 GGGACATGTCACATCGAGGAGCTCTTTAGCTCCCGGAGAAAGCTTCATGTTTC 108
DB 626905 GGGACATGTCGTCATCCAGGGTCCGGTTTCCACCCCGGAGAAAGCCAGTGTTTC 626964
QY 109 CGACCTGGGGGGCGGATGTTATCAACATGACCAACAGTTCCAGAGGTGTTCTGCTAAG 168
DB 626965 GCCGTCGGGGGTGTCATCTGTTCAACATGACCGGCTATCCGAGCGGTGCTGCTGCG 627024
QY 169 GAGGTGAATTGTTACGCA 189
DB 627025 GAACTCGAATTATGCTACGCA 627045

RESULT 15

US-09-248-796A-3979

; Sequence 3979, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3979
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3979

Query Match 20.9%; Score 39.8; DB 4; Length 738;
Best Local Similarity 55.4%; Pred. No. 9.1e-05;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 52 ACAATGGTCACATCGAGGACCTCGTTTAGCTCCCGGCGAAGCTTCATGTCCGC 111
Db 331 ACCATCATCTGTATGAGGGCCCGCAGTTTCAACCAAGCTGATCTAGATTATACAGA 390
QY 112 ACCTGGGGGGCGGATGTATCAACATGACCAAGTCCAGAGGTGTTCTTGCTAAGAG 171
Db 391 AGCTGGGGAGGTTCTGTATTAATATATGTCAGTATTGCCAGAGCCAAATTAGCTCGTGA 450
QY 172 GCTGGAATTTGTTACGCA 190
Db 451 GCAGAAATTGCTTACCAG 469

Search completed: February 1, 2005, 15:01:17
Job time : 67.497 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 13:26:09 ; Search time 261.298 Seconds
(without alignments)
4178.057 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGAATTGTTACGCAA 190

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	870	16 US-10-367-366-1	Sequence 1, Appl1
2	190	100.0	2269	18 US-10-779-476-2	Sequence 2, Appl1
3	190	100.0	2763	10 US-09-908-671-14	Sequence 14, Appl1
4	190	100.0	3083	9 US-09-780-114-1	Sequence 1, Appl1
5	190	100.0	3083	15 US-10-326-681-25	Sequence 25, Appl1
6	135.2	71.2	662	11 US-09-969-034-2820	Sequence 2820, Ap
7	119	62.6	441	9 US-09-867-701-4027	Sequence 4027, Ap
8	53.2	28.0	1029	18 US-10-653-047-7072	Sequence 7072, Ap
C 9	50.2	26.4	661	18 US-10-425-115-101607	Sequence 101607,
10	40	21.1	390	9 US-09-960-352-6576	Sequence 6576, Ap
11	35.2	18.5	870	18 US-10-873-595-53	Sequence 53, Appl
12	35.2	18.5	1418	9 US-09-782-378A-21	Sequence 21, Appl

13	35.2	18.5	1418	15 US-10-021-660-17	Sequence 17, Appl
14	35.2	18.5	1418	15 US-10-354-358-61	Sequence 61, Appl
15	35.2	18.5	1418	15 US-10-172-118-458	Sequence 458, App
16	35.2	18.5	1418	16 US-10-211-462-142	Sequence 142, App
17	35.2	18.5	1418	16 US-10-342-887-458	Sequence 458, App
18	35.2	18.5	1418	17 US-10-717-597-123	Sequence 123, App
19	35.2	18.5	1492	15 US-10-133-013-267	Sequence 267, App
C 20	34.8	18.3	16484	9 US-09-070-927A-158	Sequence 158, App
C 21	34.8	18.3	319630	16 US-10-398-221-7	Sequence 7, Appl1
C 22	34.8	18.3	3011208	16 US-10-398-221-2058	Sequence 2058, Ap
C 23	33.2	17.5	471	16 US-10-242-535A-40954	Sequence 40954, A
C 24	33.2	17.5	471	16 US-10-085-783A-40954	Sequence 40954, A
C 25	33.2	17.5	1434	16 US-10-398-221-3336	Sequence 3336, Ap
C 26	32.8	17.3	831	15 US-10-156-761-3666	Sequence 3666, Ap
C 27	32.8	17.3	9025608	15 US-10-156-761-1	Sequence 1, Appl1
C 28	31.2	16.4	507	9 US-09-878-178-1002	Sequence 1002, Ap
C 29	31.2	16.4	507	13 US-10-046-935-1002	Sequence 1002, Ap
C 30	31.2	16.4	507	14 US-10-146-502-1002	Sequence 1002, Ap
C 31	30.6	16.1	255	16 US-10-424-599-109850	Sequence 109850,
C 32	30.6	16.1	813	18 US-10-425-115-33898	Sequence 33898, A
C 33	30.2	15.9	561515	17 US-10-741-601-5682	Sequence 5682, Ap
C 34	30	15.8	293	17 US-10-437-963-20596	Sequence 20596, A
C 35	30	15.8	1257	16 US-10-343-650A-49	Sequence 49, Appl
C 36	30	15.8	1338	15 US-10-275-554-1	Sequence 1, Appl1
C 37	30	15.8	1732	15 US-10-029-656-11	Sequence 11, Appl
C 38	30	15.8	1741	9 US-09-823-245A-350	Sequence 350, App
C 39	30	15.8	1853	15 US-10-029-656-9	Sequence 9, Appl1
C 40	30	15.8	1892	16 US-10-264-237-1324	Sequence 1324, Ap
C 41	30	15.8	2119	15 US-10-037-270-35	Sequence 35, Appl
C 42	30	15.8	2119	15 US-10-117-722-35	Sequence 35, Appl
C 43	30	15.8	2171	15 US-10-241-220-47	Sequence 47, Appl
C 44	30	15.8	2171	18 US-10-872-972-47	Sequence 47, Appl
C 45	30	15.8	2171	18 US-10-872-991-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-367-366-1
; Sequence 1, Application US/10367366
; Publication No. US20040043959A1
; GENERAL INFORMATION:
; APPLICANT: Agouron Pharmaceuticals, Inc./Pfizer Inc.
; APPLICANT: Bloom, Laura A
; APPLICANT: Kuhn, Leslie
; APPLICANT: Meng, Jerry Jialun
; APPLICANT: Kung, Bei-Pei
; APPLICANT: Zehnder, Luke
; APPLICANT: Boritzki, Theodore J.
; APPLICANT: Ogden, Richard
; APPLICANT: Skallitzky, Donald
; TITLE OF INVENTION: Combination Therapies For Treating Methylthioadenosine
; TITLE OF INVENTION: Phosphorylase Deficient Cells
; FILE REFERENCE: PCI9080A (AG110-01)
; CURRENT APPLICATION NUMBER: US/10/367,366
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloned MTAP cDNA
US-10-367-366-1
Query Match 100.0%; Score 190; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 7.1e-61;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTTCTTATAGAGACTGCTAGAGACTCGGTGCCACTCAAGGACAATGCTC 60
|||||

Db 457 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAAGGGACAATGTC 516
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 120
Db 517 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 576
QY 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 577 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 636
QY 181 TGTACGCAA 190
Db 637 TGTACGCAA 646

RESULT 2

US-10-779-476-2
; Sequence 2, Application US/10779476
; Publication No. US20040247600A1
; GENERAL INFORMATION:
; APPLICANT: Leoni, Lorenzo M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF
; TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS
; FILE REFERENCE: 076936-0307942
; CURRENT APPLICATION NUMBER: US/10/779,476
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,888
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/460,715
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-476-2

Query Match 100.0%; Score 190; DB 18; Length 2269;
Best Local Similarity 100.0%; Pred. No. 9.8e-61;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAAGGGACAATGTC 60
Db 572 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAAGGGACAATGTC 631
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 120
Db 632 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 691
QY 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 692 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 751
QY 181 TGTACGCAA 190
Db 752 TGTACGCAA 761

RESULT 3

US-09-908-671-14
; Sequence 14, Application US/09908671
; Publication No. US20030138928A1
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; NOBORI, TSUTOMU
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
; DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
; TREATMENT
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/023001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 2763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Methylthioadenosine Phosphorylase (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2763

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-908-671-14

Query Match 100.0%; Score 190; DB 10; Length 2763;
Best Local Similarity 100.0%; Pred. No. 1e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAAGGGACAATGTC 60
Db 964 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCCACTCAAAAGGGACAATGTC 1023
QY 61 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 120
Db 1024 ACAATCGAGGAGCCTCGTTTAACTCCGGGCAGAAAGCTTCAATGTTCCGCACCTGGGG 1083
QY 121 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
Db 1084 GCGGATGTTATCAACATGACCACAGTTCCAGAGGTGTTCTTGCTAAGAGGCTGAATT 1143
QY 181 TGTACGCAA 190
Db 1144 TGTACGCAA 1153

RESULT 4

US-09-780-114-1
; Sequence 1, Application US/09780114
; Patent No. US20020146695A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020146695A1ori, Tsutomu
; CARSON, DENNIS A.
; TAKABAYASHI, Kenji
; TITLE OF INVENTION: Method for Detection of the Presence or
; Absence of Methylthioadenosine Phosphorylase
; (MTase) in a
; Cell Sample by Detection of the Presence or Absence
; NUMBER OF SEQUENCES: 1

;;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,114
; FILING DATE: 09-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,914
; FILING DATE: 04-May-1998
; APPLICATION NUMBER: US 08/176,855
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: US 08/459,343
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 08/827,342
; FILING DATE: 26-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-103030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3083 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3083
; OTHER INFORMATION: /note= "rat methylthioadenosine
; phosphorylase (MTase)"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 119..151
; OTHER INFORMATION: /note= "exon 1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 450..536
; OTHER INFORMATION: /note= "exon 2"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 724..782
; OTHER INFORMATION: /note= "exon 3"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 899..1066
; OTHER INFORMATION: /note= "exon 4"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1378..1480
; OTHER INFORMATION: /note= "exon 5"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1764..1953
; OTHER INFORMATION: /note= "exon 6"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2426..2548
; OTHER INFORMATION: /note= "exon 7"
; FEATURE:
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;;
; NAME/KEY: exon
; LOCATION: 2838..2876
; OTHER INFORMATION: /note= "exon 8"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-780-114-1

Query Match 100.0%; Score 190; DB 9; Length 3083;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 60
|||
DB 1764 GTTCTTATAGAGACTGCTAAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 1823

QY 61 ACAATGAGGAGACCTCGTTTACGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 120
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DB 1824 ACAATGAGGAGACCTCGTTTACGCTCCCGGCGAGAAAGCTTCATGTTCCGCACCTGGGG 1883

QY 121 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGGAATT 180
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DB 1884 GCGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGCTGGAATT 1943

QY 181 TGTTACGCCAA 190
|||||
DB 1944 TGTTACGCCAA 1953

RESULT 5
US-10-326-681-25
; Sequence 25, Application US/10326681
; Publication NO. US20030175768A1
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Schmid, Mathias
; APPLICANT: Carrera, Carlos J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Method for Early Diagnosis of, and Determination of
; FILE REFERENCE: 023070-108010US
; CURRENT APPLICATION NUMBER: US/10/326,681
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/090,411
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: genomic sequence for methylthioadenosine
; OTHER INFORMATION: phosphorylase (MTAP) gene
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(3083)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: exon
; LOCATION: (119)..(151)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (450)..(536)
; OTHER INFORMATION: exon 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: (724)..(782)
; OTHER INFORMATION: exon 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: (899)..(1066)
; OTHER INFORMATION: exon 4
; FEATURE:
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; NAME/KEY: exon
; LOCATION: (1378)..(1480)
; OTHER INFORMATION: exon 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1764)..(1953)
; OTHER INFORMATION: exon 6
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2426)..(2548)
; OTHER INFORMATION: exon 7
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2838)..(2876)
; OTHER INFORMATION: exon 8
US-10-326-681-25
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Query Match          100.0%; Score 190; DB 15; Length 3083;
Best Local Similarity 100.0%; Pred.No. 1.1e-60;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 60
          |||||||
Db      1764 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 1823

QY      61 ACAATCGAGGACCTCGTTTAACTCCCGGCGAGAAAGCTTCATGTTCCGCACTGGGG 120
          |||||||
Db      1824 ACAATCGAGGACCTCGTTTAACTCCCGGCGAGAAAGCTTCATGTTCCGCACTGGGG 1883

QY      121 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGAAGAGGCTGGAATT 180
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Db      1884 GCGGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGAAGAGGCTGGAATT 1943

QY      181 TGTTCAGCAA 190
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Db      1944 TGTTCAGCAA 1953
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RESULT 6

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US-09-969-034-2820
; Sequence 2820, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2820
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 51, 127, 216, 234, 235, 240, 289, 315, 338, 362, 365, 390,
; LOCATION: 402, 405, 410, 411, 432, 436, 442, 460, 466, 487, 493, 506,
; LOCATION: 509, 512, 525, 526, 537, 551, 560, 566, 570, 576, 581, 583,
; LOCATION: 588, 609, 611, 621, 632, 636, 649, 657
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-2820
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Query Match          71.2%; Score 135.2; DB 11; Length 662;
Best Local Similarity 90.1%; Pred.No. 3e-40;
Matches 173; Conservative 0; Mismatches 16; Indels 3; Gaps 3;
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QY      1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 60
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Db      194 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 253

QY      61 ACAATCGAGGACCTCGTTTAACTCCCGGCGAGAAAGCTTCATGTTCCGCACTGGGG 120
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Db      254 ACAATCGAGGACCTCG-TTTAGCTCCCGCAGAAAGCTTCATGTTCCGCACTGGGG 312

QY      121 GC-GGATGTTATCAACATGACCAAGTCCAGAGGTGTTCTTGT-AGGAGGCTGGAA 178
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Db      313 GCNGATGTTATCAACATGACCAANTTTCAGAGGTGGTTTGCTAAANGANGCTGGAA 372

QY      179 TTTGTTACGCAA 190
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Db      373 TTTGATACGCAA 384
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RESULT 7

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US-09-867-701-4027
; Sequence 4027, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4027
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(441)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-4027
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Query Match          62.6%; Score 119; DB 9; Length 441;
Best Local Similarity 100.0%; Pred.No. 3.4e-34;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 60
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Db      323 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCTCAAGGGGACAATGGTC 382

QY      61 ACAATCGAGGACCTCGTTTAACTCCCGGCGAGAAAGCTTCATGTTCCGCACTGGGG 119
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Db      383 ACAATCGAGGACCTCGTTTAACTCCCGGCGAGAAAGCTTCATGTTCCGCACTGGGG 441
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RESULT 8

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US-10-653-047-7072
; Sequence 7072, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
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; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7072
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-10-653-047-7072

Query Match 28.0%; Score 53.2; DB 18; Length 1029;
Best Local Similarity 61.6%; Pred. No. 2.9e-09;
Matches 85; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 49 GGGACAATGTCACATCGAGGACCTGTTTAGCTCCCGGCGAAGCTTCATGTTT 108
DB 581 GGCACATTGTTGTCATGAGGACCTCAATTTCTCACTCGCGCGAGTAAGCTTAC 640
QY 109 CGCACCCTGGGGGGGGGATGTTATCAACATGACACAGTTCAGAGTGTTCTTGTAA 168
DB 641 CGCTCTGGGGGTGGCAGCGTCATCAATGTTCTTCTTCTGAGCGAAGCTGGCTCGT 700
QY 169 GAGCTGGAATTTGTTAC 186
DB 701 GAGCCGAGATTGCTTAC 718

RESULT 9

US-10-425-115-101607/c
; Sequence 101607, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 101607
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24177C.1
US-10-425-115-101607

Query Match 26.4%; Score 50.2; DB 18; Length 661;
Best Local Similarity 62.2%; Pred. No. 3.4e-08;
Matches 79; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 64 ATCGAGGACCTCGTTTAGCTCCCGGCGAAGCTTCATGTTCCGCACTTGGGGGGCG 123
DB 309 ATGAGGGGCGCAGTTCTCGACCCGCGCGAGAGCAACCTCTACCGAGCTGGGGCATG 250
QY 124 GATGTTATCAACATGACACAGTTCAGAGGTGTTCTTGTCTAAGAGGCTGGAATTTGT 183
DB 249 GACGTCAATCGCATGACCAACATGCGGAGGCCAAGCTCGCGCGAGGCCGAGATCTGC 190
QY 184 TACGCAA 190
DB 189 TACGCGA 183

RESULT 10
US-09-960-352-6576

; Sequence 6576, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6576
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 28-LIB34-028-Q1-E1-G7
US-09-960-352-6576

Query Match 21.1%; Score 40; DB 9; Length 390;
Best Local Similarity 55.9%; Pred. No. 0.0002;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 47 AGGGACAATGTCACAAATCGAGGACCTCGTTTAGCTCCCGGCGAAGACTTCATGT 106
DB 36 AAGGACCTAATGATGTTGGGGGTCCCAATTTGAGACTGTGCGAAGTGTGCGCTGC 95
QY 107 TCCGCACCTGGGGGGCGGATGTTAATCAATGACACACAGTTCAGAGTGTTCTTGTCTA 166
DB 96 TCGGAATCTAAGGGCAGATGCTGTGTCATGACACAGTACAGAAAGTTATAGTCGCAA 155
QY 167 AGGAGCTGAATTTG 182
DB 156 GACACTGTGGAATTCG 171

RESULT 11

US-10-873-595-53
; Sequence 53, Application US/10873595
; Publication No. US20040265889A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF BIOMARKERS FOR LIVER TOXICITY
; FILE REFERENCE: D0325 NP
; CURRENT APPLICATION NUMBER: US/10/873,595
; CURRENT FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: U.S. 60/480,964
; PRIOR FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: U.S. 60/529,806
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-873-595-53

Query Match 18.5%; Score 35.2; DB 18; Length 870;
Best Local Similarity 53.7%; Pred. No. 0.017;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 47 AGGGACAATGTCACATCGAGGACCTCGTTTAGCTCCCGGCGAAGACTTCATGT 106
DB 566 AAGGACCTATGTGATGTGGCAGGCCCACTTTGAGACTGTGCGAAGTGTGCTGC 625
QY 107 TCCGCACCTGGGGGGCGGATGTTAATCAATGACACAGTTCAGAGTGTTCTTGTCTA 166
DB 626 TGCAGAACTGGAGCAGACGCTGTGGCATGAGTACAGTACAGAAAGTTATCGTGCAC 685
QY 167 AGGAGCTGAATTTG 182


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QY 47 AGGGACAATGTCACATCGAGGACCTCGTTTAGCTCCGGGACAGAAAGCTTCATGT 106
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Db 675 AAGGACCTATGTATGTGTGGCAGGCCAGCTTTGAGACTGTGCGAATGTCGTGC 734
QY 107 TCCGCACTGGGGCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTA 166
    |||||
Db 735 TGCAGAACTGGAGCAGACGCTGTGGCATGAGTACAGTACCAAGTTATCGTTGCAC 794
QY 167 AGGAGCTGGAATTG 182
    |||||
Db 795 GGCACCTGTGGAATTG 810
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RESULT 15

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US-10-172-118-458
; Sequence 458, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 458
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000270
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-458
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Query Match 18.5%; Score 35.2; DB 15; Length 1418;
Best Local Similarity 53.7%; Pred. No. 0.02;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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QY 47 AGGGACAATGTCACATCGAGGACCTCGTTTAGCTCCGGGACAGAAAGCTTCATGT 106
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Db 675 AAGGACCTATGTATGTGTGGCAGGCCAGCTTTGAGACTGTGCGAATGTCGTGC 734
QY 107 TCCGCACTGGGGCGGATGTATCAACATGACCAAGTTCAGAGGTGTTCTTGCTA 166
    |||||
Db 735 TGCAGAACTGGAGCAGACGCTGTGGCATGAGTACAGTACCAAGTTATCGTTGCAC 794
QY 167 AGGAGCTGGAATTG 182
    |||||
Db 795 GGCACCTGTGGAATTG 810
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Search completed: February 1, 2005, 17:20:50
Job time : 267.298 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 12:12:08 ; Search time 2136.25 Seconds
(without alignments)
3240.986 Million cell updates/sec

Title: US-09-780-114-1_COPY_1764_1953
Perfect score: 190
Sequence: 1 GTTCTTATAGAGACTGCTAA.....GGCTGAATTGTTACGCAA 190

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	190	100.0	509	7	CN409509	CN409509 170004239
2	190	100.0	562	7	CN409511	CN409511 170006000
3	190	100.0	580	4	BM839857	BM839857 K-EST0116
4	190	100.0	580	4	BM840883	BM840883 K-EST0118
5	190	100.0	638	7	CN409513	CN409513 170005327
6	190	100.0	738	2	BF792159	BF792159 602252620
7	190	100.0	751	7	CN409512	CN409512 170005829
8	190	100.0	813	9	AY405891	AY405891 Homo sapi
9	190	100.0	1037	4	BM903559	BM903559 AGENCOURT
10	190	100.0	1047	4	BM925551	BM925551 AGENCOURT
11	190	100.0	1064	5	BX459089	BX459089 BX459089
12	190	100.0	1075	1	AL543068	AL543068 AL543068
13	190	100.0	1380	3	BC012316	BC012316 Homo sapi
14	189	99.5	910	4	BM459757	BM459757 AGENCOURT
15	188.4	99.2	728	4	BG501032	BG501032 602546438
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17	188.4	99.2	774	7	CN409507	CN409507 170006000
18	188.4	99.2	880	5	BX374546	BX374546 BX374546
19	188.4	99.2	885	5	BX374675	BX374675 BX374675
20	186.8	98.3	838	4	BM014199	BM014199 603639894
21	185.2	97.5	694	6	CB552288	CB552288 MMSPO001
22	185	97.4	813	9	AY405892	AY405892 Pan trogl
23	183.6	96.6	764	4	BM423110	BM423110 PLATE1 GO
24	180.4	94.9	870	5	BUS09158	BUS09158 AGENCOURT

25	178	93.7	886	4	BG674546	BG674546 602620593
26	172.4	90.7	950	7	CF413058	CF413058 CH3#083 G
27	170.4	89.7	732	6	CD643696	CD643696 AGENCOURT
28	169.8	89.4	766	7	CO738989	CO738989 S1LE04c22
29	168.2	88.5	771	7	CO737569	CO737569 S1LH03c18
30	168	88.4	751	7	CN409514	CN409514 170005322
31	167.6	88.2	484	7	CF930825	CF930825 CF--05-R-
32	167.6	88.2	562	4	BI774611	BI774611 466793 MA
33	167.6	88.2	682	7	CN788377	CN788377 4122709 B
34	167.6	88.2	692	7	CK968775	CK968775 4084058 B
35	164.4	86.5	679	2	AW150875	AW150875 XG41d10..x
36	159.6	84.0	756	4	BG704891	BG704891 602688547
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38	154.8	81.5	400	1	AA221942	AA221942 mw16a04.r
39	154.8	81.5	414	7	CK391396	CK391396 K0831A05-
40	154.8	81.5	488	1	AA939482	AA939482 vz50b06.r
41	154.8	81.5	555	6	CD544714	CD544714 B0260B09-
42	154.8	81.5	620	7	CK621557	CK621557 m125g11.y
43	154.8	81.5	637	6	CD806610	CD806610 UT-M-GMO-
44	154.8	81.5	669	2	BE376457	BE376457 601226249
45	154.8	81.5	764	6	CB237920	CB237920 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS CN409509 17000423957987 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN409509
ACCESSION CN409509.1 GI:47396633
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
REFERENCE
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 509 Std Error: 0.00.
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="Oligo dt primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
ORIGIN
Query Match 100.0%; Score 190; DB 7; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 GTTCTTATAGAGACTGCTAAGACTGCTGCGGCTCAAAAGGAGCAATGTC 60
DB 181 GTTCTTATAGAGACTGCTAAGACTGCTGCGGCTCAAAAGGAGCAATGTC 240

QY	61	ACAATCGAGGGA	CCCTCGTTT	AGCTCCCGGG	CAGAAAGCTT	CATGTTCCG	CACCTGGGG	120
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QY	121	GCGGATGTTAT	CAACATGAC	CAAGTTCC	AGAGTGTT	CTTGCTA	AGAGGCTGGA	180
Db	301	GCGGATGTTAT	CAACATGAC	CAAGTTCC	AGAGTGTT	CTTGCTA	AGAGGCTGGA	360
QY	181	TGTTACGCAA	190					
Db	361	TGTTACGCAA	370					

RESULT	2
CN409511	
LOCUS	CN409511
DEFINITION	17000600010132 GRN_PREHEP Homo sapiens cDNA 5' , mRNA sequence.
ACCESSION	CN409511
VERSION	CN409511.1 GI:47396635
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 562)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,

TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

JOURNAL COMMENT
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 5622 Std Error: 0.00.

FEATURES	Location/Qualifiers
source	1. .562

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line"
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from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

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ORIGIN

Query Match	100.0%;	Score 190;	DB 7;	Length 562;
Best Local Similarity	100.0%;	Pred. No. 1.9e-50;		
Matches 190; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1 GTTCTTAGAGACTGCTAAGAAGCTAGGA CTCCGGTGCCACTCAAA GGGACAATGCTC 60
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OY	61 ACAATCGAGGACCTCGTTT TAGCTCCGGGCAGAAA GCTTCATGTTC CGCACCTGGGGG 120
Dd	242 ACAATCGAGGACCTCGTTT TAGCTCCGGGCAGAAA GCTTCATGTTC CGCACCTGGGGG 301
OY	121 GCCGATGTTATCAACATGA CCACACGTTCCAGAG GTGTTCTTGCTPA GGAAGCTGGAATT 180
Dd	302 GCCGATGTTATCAACATGA CCACACGTTCCAGAG GTGTTCTTGCTPA GGAAGCTGGAATT 361
OY	181 TGTACGCCAA 190
Dd	362 TGTTACGCCAA 371

RESULT 3					
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LOCUS					
DEFINITION	BM839857	580 bp	mRNA	linear	EST 06-MAR-2002
	K-EST0116831	SL13KMS5	Homo sapiens	cdna clone SL13KMS5-31-A07	5',
					mRNA sequence.
ACCESSION	BM839857				
VERSION	BM839857.1	GI:19196266			
KEYWORDS	EST.				
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 580)				
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,				
	Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and				
	Kim,Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Kim YS				

Genomic Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 31 row: A column: 07
High quality sequence stop: 580.

FEATURES	Location/Qualifiers
source	1. .580

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/clone_lib="S13KMS5"
/notes="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
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phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

```

ORIGIN

Query Match	100.0%;	Score 190;	DB 4;	Length 580;
Best Local Similarity	100.0%;	Pred. No. 1.9e-50;		
Matches 190; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Db 400 TGTACGCAA 409

RESULT 4
LOCUS BM840883 580 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0118036 S13KMS5 Homo sapiens cDNA clone S13KMS5-35-F08 5', mRNA sequence.

ACCESSION BM840883
VERSION BM840883.1 GI:19197292
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.kribb.re.kr
Plate: 35 row: F column: 08
High quality sequence stop: 580.

FEATURES
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location/Qualifiers
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 /clone_lib="S13KMS5"
 /notes="Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 190; DB 4; Length 580;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
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QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCGGGCGAGAAAGCTTCATGTTCCGCACTGGGGG 120
 |||||
Db 280 ACAATCGAGGAGCCTCGTTTAGCTCCGGGCGAGAAAGCTTCATGTTCCGCACTGGGGG 339

QY 121 GCGGATGTTATCAACATGACACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 180
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Db 340 GCGGATGTTATCAACATGACACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 399

QY 181 TGTACGCAA 190
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Db 400 TGTACGCAA 409

RESULT 5
LOCUS CN409513 638 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532702158 GRN_EB Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN409513
VERSION CN409513.1 GI:47396637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 638)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 638 Std Error: 0.00.

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ORIGIN

Query Match 100.0%; Score 190; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 228 GTTCTTATAGAGACTGCTAGAGAGCTAGACTCCGGTGCCACTCAAGGGGACAATGTC 287

QY 61 ACAATCGAGGAGCCTCGTTTAGCTCCGGGCGAGAAAGCTTCATGTTCCGCACTGGGGG 120
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Db 288 ACAATCGAGGAGCCTCGTTTAGCTCCGGGCGAGAAAGCTTCATGTTCCGCACTGGGGG 347

QY 121 GCGGATGTTATCAACATGACACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 180
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Db 348 GCGGATGTTATCAACATGACACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 407

QY 181 TGTACGCAA 190
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Db 408 TGTACGCAA 417

RESULT 6
LOCUS BF792159 738 bp mRNA linear EST 12-JAN-2001
DEFINITION 602252620F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4344989 5', mRNA sequence.

ACCESSION BF792159
VERSION BF792159.1 GI:12097213
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 738)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9964 row: 9 column: 06
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primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
ORIGIN
Query Match 100.0%; Score 190; DB 2; Length 738;
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Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 GCGGATGTTATCAACATGACCAACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 180
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Db 525 GCGGATGTTATCAACATGACCAACAGTTCAGAGGTGTTCTTGCTAAGAGAGCTGAATT 584
QY 181 TGTACGCCAA 190
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Db 585 TGTACGCCAA 594
RESULT 7
LOCUS CN409512 751 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700058291415 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409512
VERSION CN409512.1 GI:47396636
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,

TITLE Lebkowski,J and Stanton,L.W.
JOURNAL Transcritpome characterization elucidates signaling networks that
control human ES cell growth and differentiation
COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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Db 710 TGTACGCCAA 719
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LOCUS AY405891 813 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens MTAP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY405891
VERSION AY405891.1 GI:39761865
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 813)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 813)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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OY 61 ACAATCGAGGAGCCTCGTTTACGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 120
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OY 181 TGTACGCAA 190
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DB 631 TGTACGCAA 640

RESULT 9
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LOCUS AGENCOURT_6622141 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722000
DEFINITION 5', mRNA sequence.
ACCESSION BM903599
VERSION BM903599.1 GI:19352956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1037)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12707 row: f column: 17
High quality sequence stop: 686.
location/Qualifiers

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49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e-50;
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DB 597 ACAATCGAGGAGCCTCGTTTACGCTCCGGGAGAAAGCTTCATGTTCCGACCTGGGG 656

OY 121 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGGCTGAATT 180
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DB 657 GCGGATGTTATCAACATGACCAAGTTCAGAGGTGTTCTTCTAAGAGAGGCTGAATT 716

OY 181 TGTACGCAA 190
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DB 717 TGTACGCAA 726

RESULT 10
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LOCUS AGENCOURT_6710137 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5763749
DEFINITION 5', mRNA sequence.
ACCESSION BM925551
VERSION BM925551.1 GI:19375930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1047)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12816 row: b column: 06
High quality sequence stop: 705.
location/Qualifiers

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/note="Organ: brain; Vector: pCMV-SPORT6; site 1: NotI; site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

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Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 550 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCACACTCAAGGGAGCAATGCTC 609
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Oy 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 180
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Db 670 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 729
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Oy 181 TGTACGCAA 190
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Db 730 TGTACGCAA 739
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RESULT 11
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DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX459089 GI:47066799
VERSION BX459089.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1064)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31029072.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE012CD01QP1&c=5445.f.

FEATURES
source location/Qualifiers
1..1064
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YH01"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the
pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 100.0%; Score 190; DB 5; Length 1064;
Best Local Similarity 100.0%; Pred. No. 2.2e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCACACTCAAGGGAGCAATGCTC 60
|||||

Db 420 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCACACTCAAGGGAGCAATGCTC 479
|||||

Oy 61 ACAATCGAGGGACCTCGTTTAACTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||

Db 480 ACAATCGAGGGACCTCGTTTAACTCCCGGCAGAAAGCTTCATGTTCCGCACCTGGGG 539
|||||

Oy 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 180
|||||

Db 540 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 599
|||||

Oy 181 TGTACGCAA 190
|||||

Db 600 TGTACGCAA 609
|||||

RESULT 12
AL543068 1075 bp mRNA linear EST 24-MAR-2004
LOCUS AL543068
DEFINITION clone CS0D1002YH04 5-PRIME, mRNA sequence.
ACCESSION AL543068
VERSION AL543068.3 GI:45718631
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31264915.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5445.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1002DD02QP1&c=5445.f.

FEATURES
source location/Qualifiers
1..1075
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1002YH04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 100.0%; Score 190; DB 1; Length 1075;
Best Local Similarity 100.0%; Pred. No. 2.2e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCACACTCAAGGGAGCAATGCTC 60
|||||

Db 549 GTTCTTATAGAGACTGCTAAGAAGCTAGGACTCCGGTGCACACTCAAGGGAGCAATGCTC 608
|||||

Oy 61 ACAATCGAGGGACCTCGTTTAACTCCCGGCAGAAAGCTTCATGTTCCGCACTGGGGG 120
|||||

Db 609 ACAATCGAGGGACCTCGTTTAACTCCCGGCAGAAAGCTTCATGTTCCGCACTGGGGG 668
|||||

Oy 121 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 180
|||||

Db 669 GCGGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGGAGGCTGAATT 728
|||||

Oy 181 TGTACGCAA 190
Db 729 TGTACGCAA 738

RESULT 13
BC012316

LOCUS 1380 bp mRNA linear HTC 19-NOV-2003
DEFINITION Homo sapiens methylthiodenosine phosphorylase, mRNA (cDNA clone
IMAGE:3546198), containing frame-shift errors.

ACCESSION BC012316
VERSION BC012316
KEYWORDS GI:15147365
SOURCE HTC.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1380)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Boufard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED 22388257
REFERENCE 12477932
AUTHORS 2 (bases 1 to 1380)
TITLE Strausberg,R.
JOURNAL Direct Submission
Submitted (09-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 8 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6006025
This clone has the following problem: frame shifted.

FEATURES
source location/Qualifiers
1..1380
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3546198"
/issue_type="Placenta, choriocarcinoma"
/clone_lib="NIH MGC_21"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

ORIGIN
Query Match 100.0%; Score 190; DB 3; Length 1380;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTCTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCACTCAAGGGACAATGTC 60
Db 538 GTTCTATAGAGACTGCTAAGAGCTAGAGACTCCGGTCCACTCAAGGGACAATGTC 597

Oy 61 ACAATCAGGAGCCTCGTTTATGCTCCCGGCGAGAAAGCTTATGTTCCGACCTGGGG 120
Db 598 ACAATCAGGAGCCTCGTTTATGCTCCCGGCGAGAAAGCTTATGTTCCGACCTGGGG 657

Oy 121 GCGGATGTTATCAACATGACCACTCCAGAGGTGTTCTTGCTAAGAGCGCTGAATT 180
Db 658 GCGGATGTTATCAACATGACCACTCCAGAGGTGTTCTTGCTAAGAGCGCTGAATT 717

Oy 181 TGTACGCAA 190
Db 718 TGTACGCAA 727

RESULT 14
BM459757 910 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6417999 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534393
DEFINITION 5', mRNA sequence.
ACCESSION BM459757
VERSION BM459757.1 GI:18508797
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12220 row: m column: 18
High quality sequence stop: 679.
location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534393"
/issue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Query Match 99.5%; Score 189; DB 4; Length 910;
Best Local Similarity 99.5%; Pred. No. 4.5e-50;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
|||||
Db 531 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 590

Qy 61 ACAATCGAGGACCTCGTTTAACTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 591 ACAATCGAGGACCTCGTTTAACTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 650

Qy 121 GCGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 651 GCGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 710

Qy 181 TGTACGCAA 190
|||||
Db 711 TGTACGCAA 720

Best Local Similarity 99.5%; Pred. No. 6.7e-50;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 60
|||||
Db 249 GTTCTTATAGAGACTGCTAAGAGCTAGGACTCCGGTGCCACTCAAGGGGACAATGGTC 308

Qy 61 ACAATCGAGGACCTCGTTTAACTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 120
|||||
Db 309 ACAATCGAGGACCTCGTTTAACTCCGGGAGAAAGCTTCATGTTCCGCACCTGGGG 368

Qy 121 GCGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 180
|||||
Db 369 GCGATGTTATCAACATGACCACAGTTCAGAGGTGTTCTTGCTAAGAGGCTGAATT 428

Qy 181 TGTACGCAA 190
|||||
Db 429 TGTACGCAA 438

Search completed: February 1, 2005, 14:58:32
Job time : 2138.25 secs

RESULT 15
BG501032 728 bp mRNA linear EST 27-MAR-2001
LOCUS 602546438F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668825 5',
DEFINITION mRNA sequence.
ACCESSION BG501032
VERSION BG501032.1 GI:13462549
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1479 row: 1 column: 10
High quality sequence stop: 722.
Location/Qualifiers

FEATURES
Source 1. 728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4668825"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgctcgcc); Site_2: Sfil
(ggccatctggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.5
kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.2%; Score 188.4; DB 4; Length 728;